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-MODELE frame+ pln.model -DEV=xlp
-MODELE frame+ pln.model -DEV=xlp
-MODELE frame+ pln.model -DEV=xlp
-Q=/cgn2 1/USPTO_spool_p/US10020095/runat_15012004_163822_18707/app_query.fasta_1.1607
-DB=GenEmbl -QEMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPEX=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE-LOCAL
-OUTEMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10020095 @CGN 1 1 7794 @runat 15012004 163822 18707 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 2000000000
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1: gb_ba:
2: gb_htg
3: gb_in:
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Ygapop 10.0 , 1
Fgapop 6.0 , 1
Delop 6.0 , 1
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2888711 seqs,
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_mus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Sequence 1 from Patent WO02070696.
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Cd109 nucleic acid molecules polypeptides
Patent: WO 02070696-A 1 12-SEP-2002;
Schuh, Andre (CA); Sutherland, Robert D.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KTSLNILLI KOPKSNILLOQMLSQQSDLGVI SKTTFOLSSHELLGDMS I QVQVNDQTYYQS
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SRIVSTNVFFKQHDYI I EFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRINIVVIT
VTQRINTEYMSGSSINGGNGMEAQKI INTTVQGSTFKLEF I LEDSSELQLKAYFLGS
KSSMAYHSLETKSPSKTYY QLKTRDENI KYGSP PELLVGGNKRI KELSYNFVSRGQLVA
VGRQNSTMFSLT PENSWTPKACVI VYY I EDDGEI I SDVLKI PVQLVFKNKI KLYWSKV
VGKQNSTMFSLT PENSWTPKACVI VYY I EDDGEI I SDVLKI PVQLVFKNKI KLYWSKV
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MFMISFAVFQECGLWVLTDANLTKDY I DDVDS I TSWVATGFV I SEDLGLGLI TTTPV
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I NATGHQOTLLVPSEDGATVLFP I RFTHLGEI P I TVTALSFTASDAVTQMI LVKAEGI
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LSGFMVPSEBALSLSETVKKVEYDHGKLNILLSVANETOPCVNL FAVRHESKVI FE GFCH
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Best Local Similarity: 0 7326.50 98.82% 98.75% 99.71% Length:
Matches:
Conservative:
Mismatches: Gaps: Indels:

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781 LygVallleIleGluLysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsn 800 	dd Qy	421 ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440
61y6 6616	Qy db	401 TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420
GluL GAGC	ОУ Db	381 ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 400
	Qy Db	LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu
. 701 MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp 720 	Qy Db	341 AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 360
681 GlySerSerProHisValArgLýsHisPheProGluThrTrpIleTrpLeuAspThrAsn 700 	Qy Db	321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340
661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	ДУ	301 ABNValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 320
TTGA	Οy	281 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300
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Thre	Qγ	221 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240
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GAAA	D Q	181 SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisProlle 200
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Vals GTAT	Db Q	141 LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr 160
SerProPheGiuLeuValValSerGlyAsnLyaArgLeuLysGluLeuSerTyrMetVal	ρ δ	121 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 140
LysSerProSerLysThrTyrILeG1nLeuLysThrArgAspGluAsnIleLysValG1y) P Q	101 IleTyrGluLeuArgValThrGlyArgThrGlnAepGluIleLeuPheSerAsnSerThr 120
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533 GATATTGAAGTTGCAGCCTATGCACTCTCACACTTCTTACAATTTCAGACTT 161 GlylleProlleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheA
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081 ArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSe:
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AF410459 AF410459 AF410459 AF410 DEFINITION AF410 VERSION AF410 VERSION AF410 KEYWORDS SOURCE Homo ORGANISM Homo ORGANISM Homo Bukar REFERENCE 1 (b AUTHORS Lin, M Wu,X.	3 2	Qy 1404 Se	Qy 1384 Le	Qy 1364 II 	Qy 1344 Va Db 4193 G1	Qy 1324 G) 	Qy 1304 Le	Qy 1284 Va	Oy 1264 Pt 	Qy 1244 T) Db 3893 T/	Qy 1224 Me Db 3833 A1	Qy ·1218 Db 3773 C1	Qy 1201 G)	Qy 1181 Th
AP410459 AP410459 AP410459 AP410459 AP410459: AP41	MetGluLeuTrpleu 1428 ATGGAACTTTGGCTG 4447	SerGlySerHisHisHisSerSerValllePheIlePheCysPheLysLeuLeuTyrPhe 1423 	LeuSerSerCysAspLeuCysSerAspValGlnGlyCysArgProCysGluAspGlyAla 1403 	IlevalAspTyrTyrGluProArgArgGlnAlaValArgSerTyrAsnSerGluValLys	ValAsnIleProAlaValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSer 1363 	hrGlnPheCys 13 CCCAGTTTTGT 41	LeuSerGlyPheMetValProSerGluAlaIleSerLeuSerGluThrValLysLysVal 1323 	ValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeu 1303 	PheAspLeuAspValAlaValLysGluAsnLysAspAspLeuAsnHisValAspLeuAsn 1283 	TyrasnVallysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAla 1263 	MetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValVal 1243 	LeuAlaValValGlnPro 1223 LeuAlaValValGlnPro 1223		ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThr 1200

Cell surface antigen CD109 is a novel member of the alpha(2) macroglobulin/C3, C4, C5 family of thioester-containing proteins Blood 99 (5), 1683-1691 (2002)

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Best Local Similarity:
Query Match:
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Lin,M., Sutherland,D.R., Horsfall,W
Wu,X.-F. and Schuh,A.C.
Direct Submission-2001) Medicine, U
Submitted (14-AUG-2001) Medicine, U
College Circle, Room 7366, Toronto,
Location/Qualifiers
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Matches:
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ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 400
                                 AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG
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1101 SerProLysAlaLysGluAlaLeuAsmMetLeuThrTrpArgAlaGluGLGluGLYGLY 1120 	70TyrSerVallleArg 760	741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerValIleArg
ArgG1911eSerAspAsnTyrThrLeuAlaLeu11eThrTyrAlaLeuSerSerVa1G19	Oy 	721 ValAlaThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrThrProVal
LygTyrGLnProAsnI 1eAspVa.GInGluSerIleH1sPneLeuGluSerGluEneSer	720	701 MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp
GlyAsniysSerProValThrLeuthralaTyrIleValThrSerLeuLeuGlyTyrArg 1	700	681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsn
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1001 ProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLygGlyHis 1020 	VYZASDASDASDALAGUTYI 660 QY	
981 ABPPROSERGIYSERTHTTRPLEUSERAlaPheValLeuArgCysPheLeuGluAlaAsp 1000 	Qy 	621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal
	Qy 	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly
. LyslystysclnleuThrAspAsnLeuLyscluLysslaleuSerPheMetArgclnGly 9	Qy 	581 ThrGlnProAspSerileValGlyIleValAlaValAspLysSerValAsnLeuMetAsn
Ny	erLeuArgIleSerVal CTCTTAGGATCTCTGTG	LeuTyrTrpSerLysValLysAlaGluProSerGluLysVal
GlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGly	eLys 5	GluIleIleSerAspValLeuLysIleProValGlnLeuVal
PheSerPheProProAsmThrValThrGlySerGluArgValGln11eThrAlalle 9	Oy 	521 ProGluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGly
SerGInSerIleLeuLeuAspLeuThrAspAsnArgLeuGInSerThrLeuLysThrLeu 8	Qy 	501 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr
AlaSerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyr 8	erTyrMetVal 5 GCTATATGGTA 1	luLeuValVa AGTTGGTGGT
821 ProlleArgProThrHieLeuGlyGluIleProIleThrVelThrAlaLeuGerProThr 840	Qy 	461 LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLy
AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhe	?rSerMetAlaValHisSerLeuPhe 460	441 LeuGlnLeuLyBAlaTyrPheLeuGlySerLy8SerSerMet.
	rSerGlu 440 CAGTGAG 1432	421 ThrValProGlnSerGlyThrPheLy81leGluPheProIleLeuGluAspSe
GGTGAAGAATTIGCTTTGGAAATAACTATATTCAATTATTTGAAAGATGCCACTGAGGTT 2	Y 420	401 TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTy
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               AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG
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   ATGCAGGGCCCACCGCTCCTGACCGCCCCCCCCCTCCTGCGTGTGCACCGCCGCGCTG
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SRNVGTNVEFKOHDYLI EFFDYTTVLKESLLHTATUKVTRADGROLTLEBERRUNVUTT
VTQRUYTEYMGGSNSGNOKMEAVQKINTYTVQGGTFKI EFFILEDSSELQLKAYPLGS
KSSMAYHSLFKSPSKTYY IOLKTRDENI KVGSPFELVVSGNKRLKELSYMVVSRGQLVA
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SerSerGlu 44	420 Qy 1372 Db 2	400 CY 1312 Db 2	380 QY 1252 Db 2	360 Oy Db 2	340 Qy 11132 Db 2	320 Qy 1072 Db 2	300 Cy 1012 Db 2	280 Oy 952 Db 1	260 Cy 892 Db 1	r 240 Oy Db 1	220 Qy 772 Db 1	200 Qy 712 Db 1	180 Qy 652 pb 1	160 CY . 592 Db 1	140 Qy 532 Db 1	120 Qy 120 Db 1	100 Oy 100 Db 1	80 pb
781 LysVallleIleGluLysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsn 800	761 GlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluVal 780 	741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerValIleArg 760 	Val	MetGlyTyrArgileTyrGlnGluPheGluValThrValProAspSerIleThrSerTry	GlySerSerProHisValArgLy8HisPheProGluThrTrpIleTrpLeuAspThrAsn 	61 AlaGluArgheMetcluGluAsnGluGlyHisIleValAspIleHiaAspPheSerLeu 	41 LeuinraspalaasnLeuinrLysaspïyrlleaspGlyvalïyraspAspalaGluïyr 	TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal	01 AlaSerAsnAspileIniMeCG.uAshValValHisGluLeuGluLeuTYrAsninTody 	81 Thr 53 ACA	61 Leu 	33	73	13	81 Sea 	Ly8SerProSerLy8ThrTyrIleGInLeuLy8ThrArgAspGILA8nIleLy8ValGIy 	41 LeuGlaLeulysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 	

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01 SerProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGly 1	061 LysTyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGluSerGluPheSer 1	1001 ProfyrileAspGlnAsnValLeuHiaArgThrTyrThrTpLeuLysGlyHis 1020	1 TyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAl. TyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAl.	901 GlyAspValLeuGlyProSerTleAsnGlyLeuAlaSerLeuIleArgMetProTyrGly 920	2633 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAAGGCTGAAGAATAGAAAAATCATAT 2692 861 SerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu 880	
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361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu	11 44 55 11 44 55 11 44 55 11 44 55 11 44 55 11	141 LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr 1	Oy 101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120

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Schuh, A
                                                                    Schuh,
                                                                                                                             Homo
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Sequence 3 from
AX534936
                                                                                                                 Eukaryota;
                                                                                                                                                               AX534936.1 GI:25261478
                                                                                                       Mammalia;
                                                                                                                                       Homo sapiens (human)
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                                           ,A. and Sutherland,R.D.
nucleic acid molecules polypeptides
t: WO 02070696-A 3 12-SEP-2002;
, Andre (CA) , Sutherland, Robert D.
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Length:
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Qy 861 SerGlnSerTleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu Qy 861 SerGlnSerTleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu
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AUTHORS Schuh, A. and Sutherland, R.D. AUTHORS Gd109 nucleic acid molecules polypeptides and methods of use JOURNAL Patent: WO 02070696-A 7 12-SEP-2002; Schuh, Andre (CA); Sutherland, Robert D. (CA) EATURES Schuh, Location/Qualifiers 1.095 /organism="Homo sapiens" /mol_type="genomic DNA" /db xref="taxon:9606" CDS 1134450 /note="nunnamed protein product" /codon start=1 /codon start=1 /protein_id="CAD57234.1" /db xref="fd1.25261487" /db xref="fd1.25261487" /translation="MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTI GVELLEHCPSQVTVKAELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIY	RESULT 7 AX534940 AX534940 AX534940 DEFINITION Sequence 7 from Patent WO02070696. ACCESSION AX534940 VERSION AX534940.1 GI:25261486 KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	1424 MetGluLeuTzpLeu 1428 4433 ATGGAACTTTGGCTG 4447	1404 SerGlySerHisHisHisSerSerValllePheIlePheCysPheLysLeuLeuTyrPhe 1423 	1384 LeuSerSerCybAspLeuCysSerAspValGlnGlyCybArgProCysGluAspGlyAla 1403 	1364 IleValAspTyrTyrGluProArgArgGlnAlaValArgSerTyrAsnSerGluValLys 1383 	1344 ValAsnIleProAlaValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSer 1363 	1324 GluTyrAspHisGlyLysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCys 1343 	1304 LeuSerGlyPheMetValProSerGluAlaIleSerLeuSerGluThrValLysLysVal 1323 	1284 ValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMetGluValAsnLeu 1303 	1264 PheAspLeuAspValAlaValLysGluAsnLysAspAspLeuAsnHisValAspLeuAsn 1283 	1244 TyrAsnVallysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAla 1263 	1224 MetalavalasnileSeralaAsnGlyPheGlyPheAlaileCysGlnLeuAsnValVal 1243

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Db	TTG-
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DЬ	773 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTTGTTCT 832
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981 AspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAsp 1	Qy 961 TyrGlnArgGluLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyr 980	Oy 941 LysLysClnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMcCargGlnGly 960	921 CygGlyGluGlnAsnMetIleAsnpheAlaFrAsmIleTyrIleLeuAspTyrLeuThr	901 GJYASDVALLEUGLYPTÖSETILAASIGIYLEUALASETLEULLEAGMET FTÖLYTELY	881 SerPheSerPheProProAsnThrValThr61ySerGluArgValGLnIleThrAlaIle	861 SerGlnSerIleLeuLeuAspLeuThrAspAsnArgleuGlnSerThrLeuLysThrLeu	Qy 841 AlaSerAspAlaValThrGlmMetIleLeuValLysAlaGluGLyIleGluLysSerTyr 860	ProlleArgProThrHisLeuclyGlulleProlleThrValThrAlaLeuSerProThr	AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhe		761 GlyGluGluPheAlaLeuGluIIeThrIlePheAsnTyrLeuLysAsgAlaThrGluVal	741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerValIleArg	ValalaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThrThrProVal 	Qy 701 MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp 720		ი—բ	LeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyr 	

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Alignment Scores: Pred: No.: Score: Score: Percent Similarity: 99.91% Conservative: 1 Best Local Similarity: 99.81% Mismatches: 1 Query Match: 74.32% Indels: 0	EKSYSOŠILLDLTDNRLQSTLKTLSFSPPPNTVTGSERVQITAIGDVLGPSINGLASL IRMPYGCGEQNMINJA, PINITLDYLTKKKQLTDNLKEKALSFWRQGYQKELLYQREDG SFSAFGNYDPSGSTWLSA, FVLRCFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDP GRVIHSELQGCNKSPVTLTAYLVTSLLGYRKYQVFRI" BASE COUNT 1107 a 676 c 731 g 1021 t ORIGIN	MFMUSTAV POECGEWITDAMITKOV NOWINGARD I FIEM V REDUCTIVI OF I DE MEMOSTAV POECGEWITDAMITKOV I DOVENDAMI PARE PARENGELI TO I HOPESIGS SPHVRKHF PETWI WILDTIMESRAL POET POUT I SAVATGEVI SEDLGLGLTTTPV ELAPONOMI SENDE I LANGOHOFF I FLULF PEVENGEBERALEI I FNVIKORATSVKVI I EKSDKEDI LANGOHOFF I FLULF PER PATHLGE DET TUTPAL SPINASDAVOMI IVKAREGI INACCHORIO PER PATHLGE DET TUTPAL SPINASDAVOMI IVKAREGI INACCHORIO PER PATHLGE DET TUTPAL SPINASDAVOMI IVKAREGI INACCHORIO PER PATHLGE DET TUTPAL SPINASDAVOMI IVANI PER PATHLORIO PER	VTQRNYTEYWSGSNSGNQKMEAVQKINTTVPQSGTFKIIFFILLEUSGELQIKAYKTVIG KSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKRLKELSYMVVSRGQLVA VGKQNSTMFSLIFENSWTFAKGYIVYYIEDDGEIISVYLKIPVQLVFKNKIKLYWSKV KAFBSEKVIF DISVTTONGSVAH MANDISNATURANIVJETI EI AVETOVIC	KTSLNILIKDPKSNLIQQWLSQQSDLGVISKTPQLSSHFILGDWSIQVQVNDQTVYQS FQVSBYVLPKEEVTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVTLTPLPLSFWGK KKNITKTFKINGSANFSFIDBEMKNYNDSSNGLSEYLDLSSPGPVEILTTVTESYTGI SRNNGTNVFFKOHDY I REFPYTTVLKDSINGLSEYLDLSSPGPVEILTTVTESYTGI	/db xref="GI:25261495" /translation="MOGPPLITAPHILCVCTAALAVAPGPRFLVTAPGIIRPGGNVTI /translation="MOGPPLITAPHILCVCTAALAVAPGPRFLVTAPGIIRPGGNVTI GVELLEHCPSQVTVKAELKTASNLTVSVLEABGVPEKGSFKTLTLPSLDLNSADEIY ELRVTGRTDDEILFSNSTRLSFETKPIGVFIOTNKALVKFXGTVKFDVTFTTLFSNSKDV	CDS 1133316 /note="unnamed protein product" /codon_start=1 /protein_id="CAN57236 1"	source 13535 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"	Cd109 Patent Schuh,	Eukaryota Mammalia; 1		AX534944 AX534944 3535 bp DNA linear PAT 22-NOV-2002 DEFINITION Sequence 11 from Patent WOO2070696. ACCESSION AX534944	3293 AAGTATCAG		3173		Db 3053 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT 3112 Oy 1001 ProTyrIleAspGlnAsnValLeuHisArgThrTyrThrTxpLeuLysGlvHis 1020
321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 3	Qy 281 ThrLysThrPheLysIleAsmGlySerAlaAsmPheSerPheAsmAspGluGluMetLys 300	Qy 261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysAsnTle 280	Qy 241 MetasnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260	Qy 221 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240	Qy 201 LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 220	Qy 181 SerGlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIle 200	Oy 161 LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 180	Qy 141 LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr 160	Qy 121 ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr 140	Qy 101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120	Qy 81 GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu 100	Qy 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe 80	Qy 41 AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla 60	Qy 21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly 40	Qy 1 MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu 20	DB: Gaps: 0 US-10-020-095-4 (1-1428) x AX534944 (1-3535)

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Aichi 466-8550, Japan
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Submitted (11-MAR-2002) Department of Pathology, Nagoya University
Only of Medicine. 65 Tsurumai-cho, Showa-ku, Nagoya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hashimoto,M., Ichihara,M. and Takahashi,M. Cloning and characterization of GPI-anchored alpha-2
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SerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePhe
                                                          LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle
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                                                                                LeuSerSerProGlyProValGluIleLeuThrThrValThrGluSerValThrGlyIle
                                                                                                                                   AAGGTAATGAATTTGAAACCGCTAACGGATGTCTCGGAAGGGAGTTATGAGAATGTGGAC
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2245 TITCAGGAATGTGGTCTCTGGGTGTTGACAGATGCAACCCTTATAAGAGATAGCATTGAT 2304 653 GlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGluGluAsnGluGlyHisIle 672	593 ASPLYSSETVALASILEUMECASINALASETASILEINIMEEGIUASINVALVAHIB 61	53 LeuValPheLysAsmLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGlu 5	A BENSETTHIMET PheSETLEUTHIP PROGLUABENSETTIPTHIP PROLYBALACYBVALILE 53	ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsnLysArg 49	433 ProileLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSer	95 GlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMet 412	1360 TCAAGAATGGCAACCAATGTGTTTTTCAAGCAACATGATTACATCATTGAGATTTTT 1419 355 ASPTYTThTThTValLeuLysProSerLeuAgnPheThrAlaThrValLysValThrArg 374
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PheCysPheLysLeuLeuTyrPheMetGlu 1425
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                                                                                                           CysArgProCysGluAspGlyAlaSerGlySerHisHisHisSerSerValIlePheIle
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Klausner, R.D., Colline, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
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McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
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Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and hitial analysis of more than 15,000 full-length
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Schaetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (15-MAY-2003) National Institutes of Health, Mammalian Submitted (15-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thomas L. Casavant.
Web site: http://genome.uiowa.edu
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Proc. Natl. Acad. Sci. U.S.A. 9
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                                                                                                                                                                                                                                                                                  ocation/Qualifiers
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                                                              brain 12.5dp"
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Percent Similarity:
Best Local Similarity:
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                                                                                          ATTTATGAGCTACACATAAACGGACAATCAGAGAATGAGATCGTATTCTCCAACAGGACA
                                                                                                                IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr
                                                                                                                                                                 GluLy6GlySerPheLy8ThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu
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                      ATGCGCAGTCGGAGGCTCCTGAGCGCGGCCCACCTTCTCTGCTTGTGCGCGGGTCGCGCTG
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TSVDIE TKOPKSNVIQOMESQKEDLGVVSKTEQLUSSNPIEGDWSI QVQVNDQQYYQSF
QVLEYVLPKEEVTVQTPLYCSLKSKQLMSVI KXYTYGKPVKGSLSLTPLPLSFWGKK
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SLI RNEYGCGEQNMI YEAPNI YI LDYLTKYKYOLTUNYLKEKLSKEYRGGYORELLYQRE
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LSGFSAASDSI I LISTLKKVYEYDNGKLMI YLDSENGESVENGERSCKIL KDCSVL
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                                                                                                              TCTGTGACAGTCCACAGTATGTTCACCTCTCCTAGTAAGACGTACATCCAGCTTAAAAACC
                                                                                                                                                                                    CCAGTCATGTCCATTTCCGGCGAGCTACAACTGAAGGCTTATTTTCTTGATGGTACAAGT
                                                                                                                                                                                                                                                         GATTATATCCAGACCGTAAATTATACTATCCCCCCAAAATGGAATCATTAAGATTGAATTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCAAGAATGGCAAGCAATGTGTTTTTCAAGCATGATTACATCATTGAGATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuSerSerProGlyProValGluIleLeuThrThrValThrGluSerValThrGlyIle
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                                     AGAGATGAATATATAAAGGTGGGGTCACCTTTTGATTTGATGGTTAGTGGCAACAGACAA
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1193 GlupheAlaAlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyPro 1212	לע ממ	833 ThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeuValLys 852
ABNSETLEUGLYGLYPheAlaSerThrGlnAspThrThrValAlaLeuLysalaLeuSer	Ωy	813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832 :::::
PheLeuGlnPheGlnThrSerGluGlyIleProIleMetArgTrpLeuSerArgGlnArg	Db	793 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812
AspSerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAlaLeuLeuSerHis	рь	773 TyrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLysPheAspIle 792
1113 TrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpValSerSerGluSerLysLeuSer 1132 ::: :::	Ф	753 AsnLeuProTyrSerVallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsn 772
ThrTyrAlaLeuSerSerValGlySerProLygAlaLygGluAlaLeuAsnMetLeuThr ::: ::: TCCTATGCCCTGTCCACAGTCGGGAGCCCTAAAGCAGAGGAGGCTTTGAACTTGCTGATG TCCTATGCCCTGTCCACAGTCGGGAGCCCTAAAGCAGAGGAGGCTTTGAACTTGCTGATG	d dd	733 LeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeu 752
	da Ad	713 ValbroAspSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGly 732
ValThrSerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAsgValGlnGluSerIle ::: :::	Од	693 ThrTrpIleTrpLeuAspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThr 712
**AllieHsSerGluLeuGlInGlyGlyAsnLysSerProValThrLeuThrAlaTyrIle	od da	673 ValaspIleHisaspPheSerLeuGlySerSerProHisValargLysHisPheProGlu 692 2127 GTTGATTTTGAAGATGCTTCTTCAGTTAACAATGTACAATGTCAGGAAGAATTTTCCAGAA 2186
IntlyThrTrpLeuLySG1yH.SG1nLySSerAsnG1yG1uPheTrpAspProG1yArg	β - 54 25	653 GlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGluGluAsnGluGlyHisIle 672
LeuargCysPheLeuGluALaAspProTyrIleAspILeAspGLnAsnValLeuHisArg) B Q	633 PheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyr1leAsp 652
SerPheSerAlaPheGlyAsnTyrAspProSerGlySerThrTrgLeuSerAlaPheVal	р уу Уу	613 GluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSerPheAlaVal 632
AlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGly :::	Ф	593 AsplysSerValAsnLeuMetAsnAlaSerAsnAsplleThrMetGluAsnValValHis 612
8-1	Db .	573 LysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIleValAlaVal 592
SerLeuileArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsn 	9	553 LeuValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGlu 572 ::: ::: :::
GLUARGVALGINIJETNEALAILEGIYASDVALEUGIYPEOSETILEASNGIYLEUALA	9 dg	533 ValTyrTyrileGluAspAspGlyGluIleIleSerAspValLeuLysIleproValGln 552
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CCTGAAGGGATAGAAAAGTCGTATTCGAAATCTGTCTTATTGGATCTGACAGATAGCAAC	Db	::: ::: :::

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JOURNAL COMMENT
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                                                                                                                                                  Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY Clone from S. Wiemann, Molecular Genome Analysis, German Ca. Research Center (DKTZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University, munich/Germany) within the cDNA sequencing consortium of th
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2938)
                                                            This clone (DKFZp762L1111) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY, Email: clone@rzpd.de Further information about the clone and the sequencing project is available
                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
                                                                                                                                    Genome Project.
                                                                                                                                                                                                                                      Blum,H., Bauersachs,S., Mewes,H.W., Weil,B. and Wiemann,S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens mRNA; cDNA
AL834478
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                                http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
organism="Homo sapiens"/
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US-10-020-095-4 (1-1428) x HSM805581 (1-2938)
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                592 ValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnValVal
                 GluThrTrpIleTrpLeuAspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluVal
                                                                                                                                        AspGlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGluGluAsnGluGlyHis
                                                                                                                                                                                               ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle
                                                                                                                                                                                                                                                       HisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSerPheAla
GAGACTTGGATTTGGCTAGACACCAACATGGGTTCCAGGATTTACCAAGAATTTGAAGTA
                                                                        IleValAspIleHisAspPheSerLeuGlySerSerProHisValArgLysHisPhePro
                                                                                                                  GATGGTGTTTATGACAATGCAGAATATGCTGAGAGGTTTATGGAGGAAAATGAAGGACAT
                                                                                                                                                                                                                                                                                                 GTTGACAAAAGTGTGAATCTGAATGCCTCTAATGATATTACAATGGAAAAATGTGGTC
                                                                                                                                                                             GTCTTTCAGGAATGTGGACTCTGGGTATTGACAGATGCAAACCTCACGAAGGATTATATT
                                                                                                                                                                                                                                       CATGAGTTGGAACTTTATAACACAGGATATTATTTAGGCATGTTCATGAATTCTTTTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="melanoma (MeWo cell line)"
/clone_Tib="762 (synonym: hmel2). Vector pSport1; host
DH10B; sites NotI + SalI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="DKFZp762L1111"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHHSSVIFIFCFKLLYFMELWL'
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/db_xref="taxon:9606"
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72 IleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeuAlaLeu 10	IleValThrSerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSer 10	2 ArgVallleHisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyr 10 	1012 ArgThrTypThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGly 1031 	2 ValleuArgCysPheLeuGluAlaAspProTyrTleAspIleAspGlnAsnValLeuHis 1 	2 GlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThrTrpLeuSerAlaPhe 99 	952 LysAlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAsp 971 	932 AsnileTyrileLeuAspTyrLeuThrLysLysGlnLeuThrAspAsnLeuLysGlu 951 	912 AlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaPro 931 	892 SerGluArgValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeu 911 	872 ArgLeuGlnSerThrLeuLysThrLeuSerPheSerPheProProAsnThrValThrGly 891	852 LysalagluglyIlegluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsn 871 	832 IleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeuVal 851 	812 SerGluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIlePro 831	792 IleLeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValPro 811 	772 ASNTYrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLysBheAsp 791 	752 LeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePhe 771 	732 GlyLeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePhe 751	712 ThrValProAspSerTleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeu 731
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1415 IlePheCysPheLysLeuLeuTyrPheMetGluLeuTrpLeu 1428	1395 GlyCysArgProCysGluAspGlyAlaSerGlySerHisHisHisSerSerValllePhe 1414	1375 ValArgSerTyrAsnSerGluValLysLeuSerSerCysAspLeuCysSerAspValGln 1394 	1355 SerAsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGlnAla 1374	35 AspSerValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLysVal 	1315 SerLeuSerGluThrValLysLysValGluTyrAspHisGlyLysLeuAsnLeuTyrLeu 1334 	1295 GlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSerGluAlaIle 1314	01 G	5 ArgArgSerILeGinAsnGinGluAlaPheAspLeuAspValAlaValLysGluAsnLys	. H-v		2 FIOSEISEI 1 CCTAGCTCA	SerGlubheAlaAlaLeuMetAsnThrGluArgThrAsnTleGluValThrValThrGly	>>	152 H 681 C	132 S 621 T		092 11eThrTyra.aleuSerSerValGlySerProLysalalysGluAlaLeuAsnMetLeu [1]	441 A

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Direct Submission

Submitted (04-UUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of

Economy, Trade and Industry of Japan; CDNA full insert sequencing:

Research Association for Biotechnology (RAB); cDNA 1lbrary

construction: Helix Research Institute (HRI) (supported by Japan

Key Technology Center etc.); 5'-& 3'-end one pass sequencing: RAB,

HRI, and Biotechnology Center, National Institute of Technology and

Evaluation; clone selection for full insert sequencing: HRI and

RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
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Homo sapiens cDNA FLJ38569 fis,
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KTSLNILIKDPKSNLIQQMLSQQSDLGVISKTFQLSSHFILGDNSIQVQVNDQTYYQS
FQVSEVYLPKERVTLQTPLYCSNNSKHLINGTITAKYTYGKEVDKGDVTLTFLPLSFNGK
KKNITKTFKINGSANFS FNDEEMKNVMDSSNGLSEYLDLSS PGPVEILITVTESVTGI
SRNVSTNVFFKQHDYIIEFFDYTTVLKFSLNFTATVKVTRADGNQLTLEERKNNVVIT
VTQRNYTEYMSGSNSGNQKMEAVQKINYTVFQSGTFKLFPILEDS SELQLKAYFLGS
KSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKRLKELSYNVVSRQLVA
VGKQNSTMFSLTPENSNTPKACVIVYYIEDDGBIISDYLKIPQLVFKNKIKLYMSKV
                                                                                                                                KAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTGYYLG
MFMNSFAVFQECGLWVLTDANLTKDYIDGVYDNLFGTQEAL"
1 431 c 462 g 668 t
                                                                                                                                                                                                                                                                                                                                         /proteIn_id="BAC04642.1"
/db_xref="GI:21755237"
/translation="MOSPPLITAAHLLCVCTAALAVAPGPRPLVTAPGIIRPGGNVTI
/translation="MOSPPLITAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTI
GVELLEHCPSQVTVVAELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIY
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db_xref="taxon:9606"
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6.9e-212
3360.00
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e_lib="HCHON2"
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Length:
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                                           ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340
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                       GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT
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Unc-5 constructs and screening methods
Patent: WO 0073328-A 68 07-DEC-2000;
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                       LysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSerLysHisLeuAsn
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          AAATTTGAAGTGAATATCAAGACGTCTTCGTTTATAACTATTAAACGAT---GATTTGTCA
                                                                         -----ValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGluTyrValLeuPro
                                                                                                               GAGCTCCAACTTGCCGAAGAGACTCTCCTTGGAGATTGGTTTATCGAGGTGGAAACCTCG
                                                                                                                               ThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSerIleGlnValGln-----
                                                                                                                                                                  AGCAGAAATCTGATTTCACAGACGATTGGTGTAACTTTGGATAGAGGAGTATACAGCGGC
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553 LeuValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGlu 572	514 SETINIMELPRESELLEUINIFFOGILLASNSETTPINIFFZOLYSKALECYSVALLIEVAL 535 ::: ::: 1639 GCGACCATTAGCTTCCCAGCAACGCCTAACATGGCCCCAAAGTCACGGTTGATCGTC 1695 534 TyrTyrIleGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGln 552	ValGlySerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyr		408 GlyAsnGlnLy8MetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThr 427	370 ValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsn 387	330 SerValThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyr 349	290 AlaAsnPheSerPheAsnAspGluGluMetLysAsnValMetAspSerSerAsnGlyLeu 309	248 GlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAspValThrLeuThr 267 ::
Oy 868 LeufnraspAsnargLeuGLISETIRILEUSFIRILEUSEFRESEFRESEFFREABER 867	2674 GGAGAGATCCCGGTACATATAGCGCTATTGCATCCCAAGGTGGTGATGCAGTAGAGATG 848 MetileLeuValLysAlaGluGlyIleGluLysSerTyrSerGlnSerIleLeuLeuAsp :::: :::: 2734 AACTTGAGAGTTGATCCACAAGGATATAAAGTAGAAAATATTCCATTGTCATTGATCAATGAGAGATATAAAGTAGAAAATATTCCATTGTCAATGAC	2 ! !!		::: ::: ::: ::: ::: ::: ::: :::	2203GGTTCGTCGCCTCCACCC 696 TrpLeuAspThrAsnMetGlyTyr	Oy 648 LYSASP	62/ 1993 GAGGCAATTGATAGAAAGAAGAGGTCCATTTGGAGACCTTGGTGGGGAATTTGGAGGGAG	1816 AATGTGAAGTTTAAGGTCACATCTGACAAGAACTCTTTTGTTGGGCTTCTTGTC 593 ABPLYSSETVALASHLEUMELASHAALAGTGATAABPIIEThrMetGluASHVAlVAl :::

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                                              1225 AlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyr
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                                                                                                                                                                                                                                             AsnThrGluArgThrAsnIleGlnValThrVal---ThrGlyProSerSerProSer---
                                                                                                                                                                                                                                                                                                                                        AlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMet 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SerGluGlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPhe 1178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATGTTATTTCCCGAGCAGTCGCATTCTTGAACTCTCAACAATGGAGTCTGGTGCATTT
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                                                                                                     GATATCAACATAAGAAACGCAATTGTTCTCCAATCCTATCAACTATCTTCATTGAATGAT
                                                                                                                                                                                                      ValSerSerGlu-----SerLysLeuSerAspSer-----TrpGlnProArg 1138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATTCGAGAATTTGAAGAAACATAAGATCGTTGAGAAAAGTGGAGATGTGAAGTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaLeuAsnMetLeuThrTrpArg-----AlaGluGluGluGlyGlyMetGlnPheTrp 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGlu 1106
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Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                      van Criekinge,W., Roelens,I., Bogaert,T.
Unc-5 constructs and screening methods
Patent: WO 0073328-A 69 07-DEC-2000;
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                                         GTGTCAACAACCGCGGCGCCAGTTAAACCAGCC---ACTTATATGCTTGTCGCCCCAGCA 138
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                                                                     ValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThrAlaProGly 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCCAAGCAAACACGATCGCTGCAAGAGAAATGTGGG-----GAAGACTGTTGGCCA
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/mol type="genomic DNA"
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330 SerValThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyr 349 :::	276 LysLysAsn	228 LysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSerLysHisLeuAsn 247	172 LysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAspLeuGlyValIleSerLys 191	113GluIleLeuPheSerAsnSerThrArgLeuSerPheGluThrLysArgIleSerVal 131	55 GlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeu 74 ::::::::::::::::::::::::::::::::::::
Qy 645	2 1 1	1756 573 1816 593 1873		1399 462 1459 479 1519	Qy 388 AsnValValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSer 407
ACTTAATACACCCGGAGGTCTTACA 2172 ACTTAATACACCCGGAGGTCTTACA 2172 UTyrAlaGluArgPheMetGluGlu 667		CAAACAAGCAGTCGAGCCAGGACAG 1815 pSerIleValGlyIleValAlaVal 592 : :::::: CTCTTTTGTTGGGCTTCTTGTGGTA 1872 pIleThrMetGluAsnValValHis 612		ATATTCCTCGCTATATGTCGAGGCA 1458 ATATTCCTCGCTATATGTCGAGGCA 1458 SThrArgAspGluAsnIleLys 478 ::: GGCTGATAATGAGGGAGCTGTTGAT 1518 GGCTGATAATGAGGGAGCTGTTGAT 1518 GCTGATAATGAGGAGCTGTTGAT 1518 CCAGCCGCTGTCGACAATTACCTAT 1578 CCAGCCGCTGTCGACAATTACCTAT 1578	rGluTyrTrpSerGlySerAsnSer 407 :::::: ATACAATCATGACACTTCA 1281 nTyrThrValProGlnSerGlyThr 427 AGTTGACGCTCACGGCACCTCGGTT 1341 rGluLeuGlnLeuLysAlaTyrPhe 447 :::::: TCGCATTGAGGCTCATTATGAT 1398

795	685 HisValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsnMetGlyTyrArg 704
3616 AAAATCCAGAGCCTATATGTTCCAGGCCGTCCAGTAGACTGAAATCCAGGCCTTTATGTTCAGCCCAAATCCAGGCCTATATGTTCCAGGCCGTCCAGTAGAACTGAAACTACCTCTTTCTT	Db 3331 GATATGCAGGAGGTGCTCAGGACGGGGTGTAGCTCTAACGGCATTTGTGCTAATCTCG 3390 Qy 1056 LeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGInGluSer1leHisPheLeu 1075

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Db 4366 GATCCGGAGGAGCAGCTCAAAATGACATACGCCGCCAAGCAAAACACGATCGCTGCAAGAG 4425

Qy 1389 LeuCysSerAspValGlnGlyCysArgPro 1398

Db 4426 AAATGTGGG-----GAAGACTGTTGGCCA 4449

Search completed: January 17, 2004, 08:32:16

Job time: 11145 secs

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-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=0.5_-DELOP=6_-DELEXT=7
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Listing first 45 summaries
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-MODEL=frame+_p2n.model -DEV=xlp
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Maximum DB seq length: 2000000000
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Ygapop 10.0 , X
Fgapop 6.0 , I
Delop 6.0 , I
                                                                          January 16, 2004, 20:57:28; Search time 753 Seconds (without alignments) 5119.253 Million cell updates/sec
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1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

hila melano	ABL19704	23	6324	18.7	1376.5	45
n pregnancy z	ABQ93897	24	66	18.7	-3	44
e #3730 used t	ABN97232		5	19.1	1400	43
	AAS92193	23	4615	19.1	1400	42
ng nove	ABK92035	24	48	19.1	1401	
Drosophila melanog	ABL30183	23	4278	19.1	1406	40
quence diff	ABK63624	24	4595	19.2	1412.5	39
Human alpha-2-macr	ABS59327	24	4488	19.4	1422	38
nce encodi	AAQ11581	12	4599	19.4	1425	37
Clone encoding rec	AAQ11176	12	4569	19.4	1428.5	36
ila melan	ABL19705	23	3612	19.5	1430	35
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an al	AAH74529	22	52	9	1438	33
DNA 8	AAS94923	24	0	9	1440	32
CDNA	ABX74412	25	7	9	44	31
cDNA sequen	ABX74411	25	4578	19.6	1440	30
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n benign pros	ABK64513	24	4577	19.6	1440	27
#	ABN95738	24		9	1440	26
•	AAD45346	24		9	1440	25
DNA encodin	AAD07359		4577	19.6	1440	24
a	AAC90944	22		9.	1440	23
9	AAA52113	21	4577	19.6	1441	22
-1 proteinas	ABV77330	24	2403	19.9	1461.5	21
	AAC74484	21	5816	20.9	1533	20
secreted pr	ABA08825	22	1459	4.	1767.5	19
uman polynucleot	ABL90478	24	44	•	1819.5	18
legans alpha-	AAC90952	22	56	5		17
eqans alpha	AAC90951	22	52	25.2	1854.5	16
CD109 K15	ABQ79969	24	5	74.3	5461	15
CD109 K15 p	ABQ79968	24	53.	74.4	5470	14
r150 DNA #2	AAD49437	ა 5	19	96.2	7068.5	13
	AAD49436	25	14	96.4	7081	12
	AAA62010	21	47	99.4	7307.5	11
phobic	AAA60199	21	ω	9	7307.5	10
CD109 K1-	AB079967	24	5895	9	7317.5	9
CD109 K1 va	ABQ79965	24	76	9	7317.5	œ
platelet	AAL49816		4335	9	•	7
r150 DNA	AAD49435	25	œ		•	٥
CD109 K1-H7	ABQ79966		œ	99.7	•	U
blood cel	AAD49440		88		7326.5	44.
CD109 K1 pr	96	24	4761	99.7	7326.5	ω
platelet al	AAL49815		4335	99.7	7326.5	N
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Alignment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
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14-FEB-2002;
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                                                GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu
                                                                                                GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe
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                                                                                   GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT
                                                                                                                                   AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG
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                                     GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG
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/transl except= (pos:2132..2134, aa:/note= "Xaa corresponds to Ser, Tyr"
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                                                             LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe
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                                                                                                                                                            TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr
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             LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly
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Qy 1181 ThrGlnAspThrThrValAlaLeuLysAlaLeuLSerGluPheAlaAlaLeuMetAsnThr 1200	Qy 1161 GlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSer 1180	QY 1141 AspIleGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGlu 1160 	Qy 1121 MetGlnPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeu 1140	Qy 1101 SerProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGly 1120	Qy 1081 ArgGlyIleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGly 1100	Qy 1061 LysTyrGlnProAsnIleAspValGlnGluSerIleHisPheLeuGluSerGluPheSer 1080	Qy 1041 GlyAsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArg 1060	QY 1021 GlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGly 1040	Qy 1001 ProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHis 1020 	QY 981 AspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAsp 1000	Qy 961 TyrGlnArgGluLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyr 980	Qy 941 LysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGly 960	Qy 921 CysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr 940	Qy 901 GlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGly 920	Qy 881 SerPheSerPheProProAsnThrValThrGlySerGluArgValGlnIleThrAlaile 900	Oy 861 SerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu 880	Oy 841 AlaSerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyr 860

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RESULT 2
AAL49815
ID AAL4
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                                                                                                                           Human; platelet alloantigen; Gova; Govb; single nucleotide polymorphism; SNP; biallelic; bleeding disorder; post-transfusion purpura; post-transfusion pulatelet refractoriness; haemostatic; vaccine; neonatal alloimmune thrombocytopenia; gene; ss.
                                                                                                         Homo
                                                                                                                                                                                                                      AAL49815;
                       variation
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           /*tag= a
/product= "Gova"
/partial
/note= "no stop codon"
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PN W0200270738-A2.

XX
PD 12-SEP-2002.

XX 07-MAR-2002; 2002WO-CA00291.

XX
PR 07-MAR-2001; 2001US-273941P.

XX
PR 07-MAR-2001 SCHUH A.

XX
PR (SCHU/) SCHUH A.

XX
PA Schuh A, Ouwehand W;

XX
PI Schuh A, Ouwehand W;

XX
PI Schuh A, Ouwehand W;

XX
PI New isolated oligonucleotide binding to a region of CD109 nucleic (ACC)

XX
PT New isolated oligonucleotide binding to a region of CD109 nucleic (ACC)

XX
PT New isolated oligonucleotide polymorphism that distinguishes a Gova
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New isolated oligonucleotide binding to a region of CD109 nucleic acid having a single nucleotide polymorphism that distinguishes a Gova and/or Govb allele, useful for treating blood disorders e.g. alloimmune thrombocytopenia

Claim 6; Page 23-29; 69pp; English.

The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion platelet refractoriness or neonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Gova coding sequence.

Sequence 4335 BP; 1296 A; 837 C; 922 G; 1280 T; 0 other;

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Best Local
Query Match
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
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                    ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr
                                                                          IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr
                                                                                                                                        GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu
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GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG
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Matches:
Conservative:
Mismatches:
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01 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr 520	81 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500	AAGTCTCCTAGTAAGACTACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA 1	LysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLysValGly 4	LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 4 	421 ThrValProGlnSerGlyThrPheLyeIleGluPheProIleLeuGluAspSerSerGlu 440	TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 4	ThrieuGluGluArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 4	361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 380 	AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 3	ValGluileLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 3	301 AsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 320 	81 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300 	LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysLy	241 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260 	21 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240	01 LeuGlyAspTrpSerileGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 220	.81 SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIle 200	161 LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 180 	
Qy 861 SerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu 880	2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT	841 AlaSerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyr	Qy 821 ProIleArgProThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThr 840	Qy 801 AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhe 820	781 LysValI 2341 AAGGTAA	761 GlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluVal 	Qy 741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArg 760	Qy 721 ValalaThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrThrProVal 740	01 MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp 	681 GlySerS 2041 GGTAGCA	Qy 661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	641 LeuThrAspAlaAshLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyr 	621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal	Qy 601 AlaSerAsnAspIleThrMetCdluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620	581 ThrG1nProAspSerIleValGlyIleValAspLygSerValAsnLeuMetAsn 	561 Leutyripserlysvallysalaginproserglubysvalserleuhrgileserval	541 GluileileSerAspValLeuLysileProValGluIceuValPhety9AsnLy9ileLy9	1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGATATTATATTGAAGATGATGATGGG	

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                                                            GluArgThrAsnIleGlnValThrValThrGlyProSerSerProSerPro------
                                                                                            ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThr 1200
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CD109; alpha2 macroglobulin; thioester; cerebroprotective; c immunosuppressive; haemostatic; anticoagulant; thrombolytic; cardiovascular; vasotropic; gene therapy; CD109 K1; gene; ss
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                                                                                      CTACA
                                                                                                     LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe
                                                                                                                                                                                                                                                                                                                       ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu
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                                                                                                                                                                                ThrValProGlnSerGlyThrPheLygIleGluPheProIleLeuGluAspSerSerGlu
                                                                                                                                                                                                                               TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr
                                                                                                                                                                                                                                                                                                     ACTCTTGAAGAAAGAAGAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG
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                AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA
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                                                                                                                  Human; GPI-anchored TGF-betal binding protein; r150 protein; glycosylphosphatidyl inositol; transforming growth factor-bet therapy; blood cell syrface antigen; CD109; ds.
                                                                                                                                                                   Human blood
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24-APR-2001; 2001US-285713P
                                                                                              Homo
                       24-APR-2002; 2002WO-CA00560
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Query Match: DB:

US-10-020-095-4 (1-1428) x AAD49440

(1-5882)

Percent Similarity: Best Local Similarity:

0 7326.50 98.82% 98.75% 99.71% 25

Matches: Conservative: Mismatches: Indels:

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WPI; 2003-093100/08
                                                                   14-FEB-2002; 2002US-356163P
                                       treating
                                                              (UYMC-)
                                                              UNIV MCGILL
                                       cancer -
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Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for

Disclosure; Fig 17; 127pp; English.

The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GFI)-anchored TGF-beta binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human blood cell surface antigen, CD109 encoding DNA. CD109 is a variant of r150 sequence. Note: This sequence is stated to encode human CD109 protein shown in figure 17 of the specification, but this does not appear to be the case.

Alignment

Sequence

5882

BP;

1696 A;

1173

C; 1241 G;

1772 T; 0 other;

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                                                          LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr
                                                                                                                                                  ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC
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                                          AAGCCAAAGCAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC
                                                                                               ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr
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81 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500	441 LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 460	1 TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420	361 LysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeu 380	321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340	281 ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 300	ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 8 LYSGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle 2 LIJIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	1 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 24	S93 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 652 QY 181 SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisPxoIle 200
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TyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAla
                        ATGGCAGTTAATATTTCCGCAAATGGTTTTTGGATTTTGCTATTTTGTCAGCTCAATGTTGTA
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                                                                                                                07-MAR-2001; 2001US-273814P
                                                                                                                                                  07-MAR-2002; 2002WO-CA00292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CD109 K1-H7 protein encoding cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activation, increased or impaired activation of the coagulation and/or fibrinolytic systems, or impaired or increased immune activation. These are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, thrombocytopenia, thrombocythemia, autoimmune diseases, organ transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for their antisense conditions. The present sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and activation, increased or impaired the coagulation and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful to the protein and the containing proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5895 BP; 1709 A; 1173 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating these conditions. CD109 K1-H7 cDNA sequence.
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                                                                                                                                                 IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120
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                                                                                                                         ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC
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520	ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr	501	8
500 1612	SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal	481 1553	유 성
480 1552	IleGlnLeuLysThrArgAspGluAsnIleLysVal 	461 1493	B &
460 1492	LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe 	441 1433	B 8
	sIleGluPheProIleLeuGluAspSerSer 	421 1373	유 성
ωŅ	nGlnLysMetGluAlaValGlnLysIleAe 	401 1313	₿ &
400 1312	ThrieuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGlu 	381 1253	유 성
380 1252	LysProSerLeuAsnPheThrAlaThrValLysValThrArġAlaAspGlyAsnGlnLeu 	361 1193	유 성
360 1192	ASNValPhePheLySGlnHisAspTyr1leIleGluPhePheAspTyrThrThrValLeu	341 1133	유 성
340 1132		321 1073	B 8
320 1072	AsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGlyPro 	301 1013	유 성
300 1012	ThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys	281 953	유왕
280 952	LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysLysAsnIle 	893	유 성
260 892	MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 	241 833	B 8
240	ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 	221 773	유 성
220 772	LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 	201 713	유 성
200 712	SerGlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIle	181 653	B 성
180 652	LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu 	161 593	B 8
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Qy 821 Proi Db 2573 CCCA Qy 841 Alas Db 2633 GCTT Qy 861 SerG Qy 861 SerG Qy 861 SerG Db 2693 TCAC	Qy 781 Lys Db 2453 AAC Qy 801 Ala Db 2513 GCC	741 2333 761 2393	Qy 701 Met Db 2213 ATC Qy 721 Val Db 2273 GT	Qy 661 Ala Db 2093 GC7 Qy 681 G1 Db 2153 GG7	Qy 621 Tyy Db 1973 TA: Qy 641 Le Db 2033 TT	1853 601 1913	561 1793 581	Qy 541 Gl Db 1673 CC2 Qy 541 Gl Db 1733 GAA
IleArgProThrHisLeud	LysVallleIleGluLysSerA	LeuGlnAlaPheGlnProp	GlyTyrArgileTyrGlnG	AlaGluArgPheMetGluGluA	TyriouglyMetPheMetA		euTyrTrpSerLysValLysA TATATTGGAGTAAAGTGAAAG	
ProIleArgProThrHisLeuGlyGluIleProIleThrValThrAlaLeuSe	uLysSerAspLysPheAspIleLeuMetThrSerSerGl	GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerVal	MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp	AlaGluargPheMetGluGluasnGluGlyHisIleValAspIleHisAspPheSerLe	TYTTYTLEUGLYMET PheMet AsinSerPheAlaVal PheGlinGlinGysGlyLeuTrpVall	ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGAATCAAT AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly	rTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 	FIGGLIASDSETITPINTFTOLYSALACYSVALLLEVALTYTYTLEGILASDASDGIN
USERPROTHE 	erGlulleAsn :: aTGAAATAAAT hrValLeuPhe 	erVallleArg	SerTrp	∪—¤ ⊕—¤	TrpVal		eSerVal	TGATGGG SIleLys
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	AspileGluvalalaalaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGlu	SerProLysAlaLysGluAlaLeuAsnMetLeuThrTrpArgAlaGluGluGluGlyGly		CAGAAATCCAACGGTAACTTACAGCCTATATTGTAACTTCTCTCCTGGGATATAGA GGCAATTAAAAGTCCAGTAACTTACAGCCTATAGTGAACTTTAGAGG GGCAATTAAAAGTCCAGTAACACTTACAGCCTATAGTGAGCTTCAAGGT GGCAATTAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCTCTC		AAAAAGAAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT TYTG1nArgG1uLeuLeuTyrG1nArgG1uAspG1ySerPheSerA1aPheG1yAsnTyr	CysGlyGluGlnAsnMetileAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr 	AGTITCTCATTICCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT AGTITCTCATTICCTCCTAATACAGTGACTGGCCAGTGAAAAGAGTTCAGATCACTGCAATT G1yAspValLeuG1yProSerIleAsnG1yLeuAlaSerLeuIleArgMetProTyrG1y
AGGCTICTTCCTTC	JEGCTCT	AsnMetLe	SINGIUSEI CAAGAGTCT CEUAlaLet	ASPERGEL ATCCAGGE ThrAlaTy ACAGCCTAI ACAGCCTAI	CAGCTTT	TTGAAAGAA ArgGluAsp AGGGAAGA1	PheAlaPro	HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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RRSULT 6
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glycosylphosphatidyl
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                                         2002WO-CA00560
                                                                                                                                                                                                                                                                                              /product= "Human r1520 protein #2"
/transl_except= (pos:2219..2221, a
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein
                                                                                                                                                                                                                                                                     Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-093100/08.
P-PSDB; AAE32013.
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14-FEB-2002; 2002US-356163P.
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Sequence 5883 BP; 1696 Α; 1173 Ç 1241 G; 1772 T; 1 other;

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LysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeu
                                           LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr
                                                                       IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr
                                                                                                                                                                       GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu
                                                                                                                                                                                                                                                      AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla
                                                                                                                 ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC
                                                                                                                                                           GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT
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Qy 521 Db 1673	Qy 501 Db 1613	Qy 481 Db 1553	Qy 461 Db 1493	Qy 441 Db . 1433	Qy 421 Db 1373	Qy 401 Db 1313	Qy 381 Db 1253	Qy 361 Db 1193	Oy 341 Db 1133	Оу 321 Db 1073	Qy 301 Дb 1013	Qy 281 Db 953	Qy 261 Db 893	ü	Qу 241
ProGluAsnSerTrpThrP CCAGAAAATTCTTGGACTC	ValSerArgGlyGlnLeuValAla 	SerProPheGluLeuValV TCGCCTTTTGAGTTGGTGG	LysSerProSerLysThrT AAGTCTCCTAGTAAGACAT	LeuGlnLeuLysAlaTyrPheI CTACAGTTGAAGGCCTATTTCC	ThrValProGlnSerGlyT	TyrTrpSerGlySerAsnS 	hrLeuGluGluArgArgA 	LysProSerLeuAsnPheT 	AsnValPhePheLysGlnH AATGTGTTCTTCAAGCAAC	ValGluIleLeuThrThrV gTaGAAATTTTAACCACAG	AsnValMetAspSerSerA	ThrLysThrPheLysIleA ACAAAAACATTTAAGATAA	LysGlyAspValThrLeuT 	MetAsnSerLysHisLeuA ATGAATTCTAAGCATTTAA	
ProLysAlaCysVallleValTyrTYrIleGluA CCAAAAGCCTGTGTAATTGTGTATTATATTGAAG	ıValGlyLysGln GTAGGAAAACAA	alValSerGlyAsnLysArgLe GGTTAGTGGCAACAAACGATT	/9ThrTyrIleGlnLeuLy8ThrArgAspGluA 	heLeuGlySerLysSerSerMetAlaValHiss TCCTTGGTAGTAAAAGTAGCATGGCAGTTCATA	SerGlyThrPheLysIleGluPhePr 	rGlySerasnSerglyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 	ThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGl 	.gn.pheThralaThrVallysValThrArgAlaAspGlyAsnGlnLeu 	ysGlnHisAspTyrIleIleGluPh aGCAACATGATTACATCATTGAGTT	eLeuThrThrValThrGluSerValThrGlyIleSerArgAsnVa 	erSerAsnGlyLeuSerGluTyrLeuAsp 	PheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLys 	pValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLy 	SLeuasnGlyThrIleThralaLysTyrThrTyrGlyLy 	
ATG:	AsnSerThrMetPheSerLe AATTCAACAATGTTCTCTTT	euSerT	snIleLy ATATAAJ	:rMetAlaValHisSerLeuPhe CATGGCAGTTCATAGTCTGTTT	/BIleGluPheProIleLeuGluAspSerSerGlu 	.uAlaValGlnLysIleAs AGCTGTTCAGAAAATAAA	lThrGlnArgAsnTyrTh GACACAGAGAAACTATAC)rArgAlaAspGlyAsnGl TCGTGCTGATGGCAACCA	.eIleGluPhePheAspTyrThrThrVa CATTGAGTTTTTTGATTATACTACTGT	8—1s	:uAspLeuSerSerProGlyP GGATCTATCTTCCCCTGGAC	erPheAsnAspGluGluMe 	ETrpGlyLysLysLysAs TTGGGGAAAGAAGAAAAA		
pGly 540 NTGGG 1732	euThr 520 AACA 1672	YrMetVal 500 NTATGGTA 1612	/sValGly 480 \GGT0GGA 1552	uPhe 460 GTTT 1492	440 TGAG 1432	ITYF 420 	irGlu 400 TGAG 1312	nLeu 380 ACTG 1252	#lLeu 360 rCTTG 1192	erThr 340 CACT 1132	.YPro 320 ;ACCA 1072	ELYS 300 GAAA 1012	/sAsnIle 280 NAAATATT 952	3ProVal 260 CCAGTG 892	
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SerPheSerPheProProAsnThrVa 		AlaSerAspAlaValThrGlnMetI	ProIIeArgProThrHisLeuGlyG 	A Latin'd yet signification and a control of the co	LysVallieTleGluLysSerAspiz 	HIGHUPHEALALEUGIUILETE	3AGCTCCAAGCCTTCCAACCATTTTTTTTTTTTTTTTTTT	ValAlaThrGlyPheValIleSerG	MetGlyTyrArgIleTyrGlnGluPi ATGGGTTNCAGGATTTACCAAGAAT	GlySerSerProHisValArgLysH:	AlaGluArgPheMetGluGluAshG 	LeuThrAspAlaAsnLeuThrLysAs	TATTATTTAGGCATGTTCATGAATT	GCCTCTAATGATATTACAATGGAAAA	
SerPheSerPheProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIle 	H-0	AlaserAspalaValThrGliMetIleLeuValLysAlaGluGlyIleGluLysSerTyr	ProlleArgProThrHsBeeuGlyGluIleProlleThrYalThrAlaLeuSerProThr 	A TATING LYH SGING INTINLEULEUWA LY POSETGIUASDGI YATATIN WALLEUPIE GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT	Lysvalile ileglulysseraspilyspheaspile LeuwethnSerSerGluileAsm 	GlyGluGluPhaAlaLeuGluILeThrIlePhaAsnTyrLeuLygAspAlaThrGluVal	GluLeuGIRALAPheGIRPTOPREPRELLEPRELLASHLEUPTOTYPTSETVALILEATE	ValAlaThrGlyPheValI168erGluAspLeuGlyLeuGlyLeuThrThrThrProValI	MetGlyTyrArg1leTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp	GlySerSerProHisValArglysHisPheProGluThTTpIleTrpLeuAspThrAsn 	AlaGLIMITSPheMetGLUGLUAHNGLUGLYHIBILEVALASDILEHISASDPheSerLeu 	LeuthraspalaasnLeuthriysaspTyrIleAspGlyValTyrAspAsnAlaGluTyr	YFIYTHEUGIYMETERAMSETERAA AVAIRREGINGYSGIYHEUITYVAI		

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                                                                                                                                          GluArgThrAsnIleGlnValThrValThrGlyProSerSerProSerPro------
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TyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAla 126:
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                                                                           CTGATTGACACACACACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGTGGTACAGCCA
                                                                                         -----LeuAlaValValGlnPro
                                                                                                                           GAAAGGACAAATATCCAAGTGACCGTGACGGGCCTAGCTCACCAAGTCCTGTAAAGTTT 3772
                                                                                                                                                                             ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA
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Human; platelet alloantigen; Gova; Govb; single nucleotide polymorphism; SNP; biallelic, bleeding disorder; post-transfusion purpura; post-transfusion platelet refractoriness; haemostatic; vaccine; neonatal alloimmune thrombocytopenia; gene; ss.
                                                                                                                                                                                                                                                                                                                                        Human platelet alloantigen Govb coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetGluLeuTrpLeu 1428
||||||||||||
ATGGAACTTTGGCTG 4447
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Alignment
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion platelet refractoriness or neonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Govb coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated oligonucleotide binding to a region of CD109 nucleic acid having a single nucleotide polymorphism that distinguishes a Gova and/or Govb allele, useful for treating blood disorders e.g. alloimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim
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                                                                                     LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTy
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New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
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Claim 1; Fig 1b; 156pp; English.

CC The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioseter-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes and of the complement system, quantitative or qualitative abnormalities CC of platelet function, increased or impaired platelet aggregation and CC activation, increased or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired activation of the coagulation and/or CC transplantation, or bone marrow transplantation ard isease, cc transplantation, or bone marrow transplantation. The CD109 nucleic acids CC or their antisense nucleotide sequence are useful in gene therapy for treating these conditions. The present sequence represents the human CC CD109 KI variant CDNA sequence.

Sequence 4761 1419 A; 913 ç 1016 G; 1413 T; 0 other;

Scores:

Best Local Si Query Match: DB: S 밁 Ś 밁 Ś 밁 S 밁 S 밁 Ś 멍 Ś 밁 á US-10-020-095-4 (1-1428) x ABQ79965 (1-4761) Percent Similarity: No.: 121 141 473 413 101 353 293 233 173 113 81 61 41 Similarity: 21 \vdash ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu LysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyr IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120 **AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG** AsnValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAla GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGGCCCCGGAGGA ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGCACCGCCGCGCTG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT 0 7317.50 98.75% 98.69% 99.58% 24 Gaps: Length: Matches: Conservative: Mismatches: Indels: 4761 1426

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AAGCCAAAGCAAGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC

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CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human; cardiovascular; vasotropic; gene therapy; CD109 K1-H7; variant; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 Cf family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired or increased immune activation. These calso useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, organ thrombocytopenia, thrombocythemia, autoimmune diseases, organ cortivation these conditions. The present sequence represents the human cc CD109 K1-H7 variant CDNA sequence.
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y Match:
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     TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA
                       SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal
                                                                           AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA
                                                                                               LysSerProSerLysThrTyrI1
                                                                                                                                             CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT
                                                                                                                                                                   LeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPhe
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1218LeuAlaValValGlnPro 1223	Qy	ACCCAGATGATTTTAGTAAAAGGCTGAAAGGAATAAAAAAA
1201 GluArgThrAsmIleGlnValThrValThrGlyProSerSerProSerPro 1217	Db Qy	841 AlaSerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyr 86
653 ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA 37	Db	821 ProIleArgProThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThr 840
3593 GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT 3652 1181 ThrGlnAspThrThrValAlaLeuLvsAlaLeuSerGluPheAlaAlaLeuMetAsnThr 1200	δ B	2513 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT 2572
3533 GATATTGAAGTTGCAGCCTATGCACTGCTCTCACACTTCTTACAATTTCAGACTTCTGAG 3592 1161 GlylleProlleMctArgTrpLeuSerArgGlnArgAanSerLeuGlyGlyPheAlaSer 1180	QQ DB	Alambarananan 2
AspIleGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGlu	Q	AAGAATTTGCTTTGGAAATAACTATATTCAATTTATTTGAAAGATGCCACTG allleileGluLysSerAspLysPheAspIleLeuMetThrSerSerGluI
1121 MetGlnPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeu 1140	당성	1 GlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluVal
HIII	D	741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArg 760
ATGG191 ESETABDABILYTINILEUALALEULTETHTIYATALALEUSETSETVAIGIY I	B. 5	721 ValalaThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrThrProVal 740
OS. 1987) TGIRFTOABRILEASDVALGINGIUSET LEHISFRELEUUTUSETGIUFRESET 1987) B 6	701 MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp 720
GIVASHAYASEEFE CAAIIII LEGUIITAA AYYILEGA TAATAA AAGAA AAGAAA AAGAA AAGAAAAAA) B 6	681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsn 700
CAGAAATCCAACGGTGAATTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT 323	?	661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680
.001.FT01YT1EASD11EASD41MSDVALLEUH1SATG1MTYTIMTTTDLEULYSG1YH1S 113 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3	B &	641 LeuThTASpAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyr 660 2033 TTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTTATGACAGATGCAGAATAT 2092
B1 ASPPROSEZGLYSETINTITELEUSERALBENEVALLEUARGCYSENELEUGIUALAASP 1	?	621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal 640
61 TyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyr 9	2 4 4 6	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620
41 LyslysLysCinLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgCinGly 9	Db Q	581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600
CysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr	D	561 LeuTyrTrpSerLysValLysAlaGluProSerGlüLysValSerLeuArgIleSerVal 580
GlyAsgValLeuGlyProSerIleAsmGlyLeuAlaSerLeuIleArgMetProTyrGly	dg dg	541 GluileileSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560
SerPheSerPheProProAsmThrValThrGlySerGluArgValGln1leThrAlaIle	ob Q	521 ProGluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGly 540
SerGinSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu 8	Qy da	501 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr 520

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                                                                                                                                                                                                             Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopolesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;
                          17-NOV-1999;
                                                                  25-MAY-2000.
                                                                                                         WO200029448-A2
                                                                                                                                                                                                                                                                                                                                                                 Hydrophobic domain protein cDNA HP02837 isolated from HT-1080 cells
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Best Local Similarity:
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22-DEC-1998;
16-MAR-1999;
27-APR-1999;
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P-PSDB; AAB12127.
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                                                                                                                                                        GluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGlu
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  ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr
                                                                    IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr 120
                                                                                                                                                                                                                 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT
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Secretory proteins play important roles in the proliferation control, the CC differentiation induction, the material transport and the biophylaxis of CC ells. Membrane proteins have important roles as signal receptors, ion CC channels and transporters. The present sequence is the coding sequence CC for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell cprotein. The encoded protein activity, immune stimulating or suppressing activity, haematopoiseis activity, immune stimulating or suppressing activity, haematopoiseis activity, tissue growth activity, haemostatic and thrombolytic activity, anti-inflammatory activity and tumour cinhibition activity, anti-inflammatory activity and tumour treatment of autoimune disease, Alzheimer's disease, Parkinson's clisease, and cancer via gene therapy.
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hemostatic, thrombolytic -
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841 AlaSerAspAlaValThrGinMetILeLeuValLysAlaGluGlyTleGluLysSerTyr 860 :::	Db Cy	481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500 	¥
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alyGluGluPheAlaLeuGluIleThrIlePheAsmTyrLeuLysAspAlaThrGluVal	d dd y	401 TyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyr 420 	ъ ч
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AAA62010 standard; DNA;

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entry)

Hydrophobic domain protein cDNA HP02837 isolated from HT-1080

cells.

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XX Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolyric; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer;

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22-DEC-1998;
16-MAR-1999;
27-APR-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, the condition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer via gene therapy.
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                        AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAAATATAAAGGTGGGA
                                                                           CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAGTAGCATGGCAGTTCATAGTCTGTTT
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1201 GLUARGTHRASHILEGINVAITHRVAITHRGIVEROSERSERPROSERPRO 1217	- da Ab	841 AlaSerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyr 860
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GJYLIEFTOILEMECATGITDLEUSEKATGASINSELUGIAYALYENGA ASEL	D 5	801 AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhe 820 [
AppileGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGlu 1	o dd Qy	781 Ly8VallleIleGluLy8SerAspLysPheAspIleLeuMetThrSerSerGluIleAsn 800
MetGlnPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeu	. pb	GlyGluGluPheAlaLeuGluIleThrIlePheAsnTyfLeuLysAspAlaThrGluVal
1101 SerProLysAlaLysGluAlaLeuAsnWetLeuThrTrpArgAlaGluGlnGluGlyGly 1120 	Qy Db	
ylleSerAspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGly 	Qy db	ValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThrProVal 7
1061 LysTyrGlnProAsnIleAspVelGlnGluSerIleHisPheLeuGluSerGluPheSer 1080 	Qy Db	MetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrp ATGGGTTCCAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG
GlyAsnLysSerProValThrLeuthrAlaTyrIleValThrSerLeuLeuGlyTyrArg 1 	Qу	-
GlnLysSerAsnGlyGlubheTrpAspProGlyArgVallleHisSerGluLeuGlnGly 104	Q y Db	
ProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHis	Qу	
AgproSerGlySerThTTpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAsp 	Qy Db	621 TyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpVal 640
TyrGlnArgGluLeuLeuTyrGlnArgGluAepGlySerPheSerAlaPheGlyAsnTyr 	Db Qy	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly 620
LysLysGInLeuThrAspAsnLeuLysGInLysALaLeuSerPheMetArgGInGly	dd Q	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn
CysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr	Qy Db	
901 GlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGly 920	Qy Db	GluileileSerAspValleuLysileProValGlnLeuValPheLysAsnLysileI
SerPheSerPheProProAsmThrValThrGyySerGluargyalGinlleThrAlaile	D QQ	521 ProGluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGly 540
TCACAATCCATCTTATTAGACTTGACTGACAATAGGCTACAGAGTACCCTGAAAACTTTG	da Vy	501 ValSerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetPheSerLeuThr 520
GCTTCTGATGCTATCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT 2	- B	

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                                                                                                                                                                                                             cell surface antigen,
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/*tag= a
/produce "Human CD109 protein"
/transl_except= (pos:2044..2046,
/note= "Xaa corresponds to Ser, T
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Alignment
                                                       The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human blood cell surface antigen, CD109 encoding DNA. CD109 is a variant of r150 sequence.
                                                                                                                                                                                                                                                                      Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
                               Sequence 4146 BP;
                                                                                                                                                                                                                          Claim 7; Page 109-112; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-2001;
14-FEB-2002;
                                                                                                                                                                                                                                                          treating cancer
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2002US-356163P.
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DB: Š 밁 Ş 밁 Ś 맑 Ś Score: US-10-020-095-4 (1-1428) x AAD49436 No.: 121 82 62 61 42 22 LysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIle CTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTTGAA LeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPheGlu GTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCGGAG ValThrIleGlyValGluLeuLeuGluHisCysProSerGlnValThrValLysAlaGlu 0 7081.00 99.86% 99.78% 96.37% 25 (1-4146)Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 4146 1379 1 0

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ProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyrLys

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LeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLys

TTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCAAACAGACAAGGCCTTATACAAG

TyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArg

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ANAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAGATT

TATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACCCGC

SerArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThrMetpheSerLeuThrPro 521 	GluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetValVal 50 	2 SerProSerTysThrTyr1leGlnLeuLysThrArgAspGluAsn1leLysValGlySer 4	GInLeuLysalaTyrPheLeuGlySerLysSerSerMetAlaValHisSerLeuPheLys 46	ValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGluLeu	2 TrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyrThr 421	2 LeuGluGluArgArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGluTyr 4	2 ProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeuThr 3	ValLeuLys 3	GlulleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThrAsn []	ValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerBroGlyProVal 32	LyGThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMetLysAsn 30	39ValThrieuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIlleThr 	2 AsnSerLysHisLeuAsnGlyThrlleThrAlaLysTyrThrTyrGlyLysProValLys	SerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMet	CARRELES (118978) CALLE COMMENT AND CALLES (1887) CARRELES (1887) CALLES	2 GlnGlnSerAspLeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeu	ThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSer 18
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882 PheSerPheProProAsnThrValThrGlySerGluArgValGhnIleThrAlaileGly 901	42 SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSer 8	822 IleargProThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAla 841 	802 ThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhePro 821 	782 ValileīleGluLysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAla 801 	762 GluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLys 781 	742 LeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArgGly 761 	722 AlaThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrThrProValGlu 741 	702 GlyTyrArgileTyrGlnGluPheGluValThrValProAspSerIleThrSerTzpVal 721 	682 SerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsnMet 701 	662 GluargPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeuGly 681	642 ThraspalaasmLeuThrLysaspTyrIleaspGlyValTyrAspAsmAlaGluTyrAla 661 	622 TyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeu 641	602 SerasnabpileThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGlYTyr 621 	582 GlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAla 601 	562 TyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThr 581 	542 IleIleSerAspValLeuLysIleProValGInLeuValPheLysAsnLysIleLysLeu 561 	522 GluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGlyGlu 541

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Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; gene; ds.
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SerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMet
                                                        GlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnVal
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                                                                      TyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThr
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                                         The invention relates to isolated nucleic acid molecules encoding CD109 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 KI, CD109 KI-T, CD109 KI5 or their variants. CD109 is a novel member of the alphaz macroglobulin (alphazM)/C3, C4, C5 family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                            New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes
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                                                                                                                                                                   Claim 1; Fig 4a;
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                                                 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer
                                                                                                             LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln
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MetGlyTyrArgIleTyrGlnGlubheGluValThrValDroAspSerIleThrSerTrp 7) D Q	341 AsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrValLeu 360 	B &
	ДУ	321 ValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAsnValSerThr 340 	β δ
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The invention relates to isolated nucleic acid molecules encoding CD10 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 E1-H7, CD109 K15 or their variant CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, Eamily of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful for treating or detecting a disease or disorder, e.g. conditions
                                                                                                                                                              New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thromit thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
                                                                                                                               Claim 1; Fig
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                                                                                                                                                                                                                                                                                                             IleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThr
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                   LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln
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   TCACAACAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA
                                                                                                                    ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC
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541 GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560	481 SerProPheGluLeuValValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetVal 500	421 ThrValProGlnSerGlyThrPheLysIleGluPheProIleLeuGluAspSerSerGlu 440	CCATCTCTCAACTTCACAGCCACTGTGAA LeuGluGluArgArgAsnAsnValValII.	ValGluIleLeuThrThrValThrGluSerValThrGlyIleSe	241 MetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProVal 260
Db 2813 GGAGATGTTCTTGGTCCATCAATGGCTTAGCCTCATTGATTCGGATGCCTTATGGC 2872 Qy 921 CysGlyGluGlnAsnMetlleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThr 940	2633 861 2693 881 2753	2453 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTCTTCAAATGAAATTAAAT 801 AlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPhe	741 GluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArg 760	Oy 681 GlySerSerProH.8ValArgLy8818PheProGulThrTtpIleTpLeuAspThAAsn 700	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGly

8	2993	
ş	981	AspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAsp 1000
Ъ	3053	053 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT 3112
γŞ	1001	ProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeuLysGlyHis 1020
B	3113	CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3172
δ	1021	1021 GlnLysSerAsnGlyGluPheTrpAspProGlyArgVallleHisSerGluLeuGlnGly 1040
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γQ	1041	1041 GlyAsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArg 1060
₽	3233	GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACCTTCTCCTCGGGATATAGA 3292
Ş	1061	1061 LysTyrGln 1063
문	3293	AAGTATCAG 3301

Search completed: January 17, 2004, 01:15:04 Job time : 983 secs

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Command line parameters:

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-LIST=45 -DOCALIGN=200 -THR SCORE=pot -THR MAX=100 -THR MIN=0 -ALIGN=15
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               US-09-241-606-1

US-09-016-434-1174

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US-08-793-126-2

US-09-132-271-2

US-09-132-271-2

US-09-132-27-1

US-09-62-227-1

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Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli	equence 322 equence 256 equence 5, equence 5,	1, 7 1, 7 243, 60, 78,	3, Appl e 10214, e 9, Appl e 1360, App e 237, App e 261, App e 265, App e 265, App e 27, App e 27, App e 21, App	Sequence 1090, Ap Sequence 1, Appli Sequence 3, Appli Sequence 56, Appl

ALIGNMENTS

RESULT 1 US-09-241-606-1

Sequence 1, Application US/09241606 Patent No. 6472140

GENERAL INFORMATION:

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Percent Similarity:
Best Local Similarity:
                                                                                Alignment Scores:
                                                                                                                US-09-241-606-1
                                                                 Pred. No.:
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APPLICANT: Kovace, Dora
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods for
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 0609.4460003
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CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
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NAME/KEY: sig_peptide
LOCATION: (44)..(112)
                                                                                                                             NAME/KEY: mat_peptide LOCATION: (113)..(4468)
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LOCATION: (44)..(4468)
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B & B & B & B & B & B & B & B & B & B &	D
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Alignment Scores:
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                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                 NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                        TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for v
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Zeller, Karen J.
                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
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                                                                                                                          STRANDEDNESS:
                                                                                                                                               LENGTH: 4079 base pairs
TYPE: nucleic acid
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Best Local Similarity:
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917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936 :::	Y 897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916 :::::: ::: :::::: 2885 GTCTCAGTTTTGGGAGACATATTAGGCTCTGCCATGCAAAACACACAAAATCTTCTCCAG 2944	877 LeulysThrieuSerPheSerPheProProAsmTnrValThrGlySerGluArgValGln	857 GlulysSerTyrSerGlnSerTleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr	842	833 ThrValThrAlaLeu ::: 2654 ACTGTGAGCGCAGAG	y 813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832	798 2567	y 778 ThrGluValLysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797	758 VallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla	y 738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757	718 ThrSerTryValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr	698 ASpThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle	681 GlySerSerÞroHisValArglysHisPheProGluThrTrpIleTrpLeu	2168 GAGTCAGATGTAATGGGAAGAGGCCATGCACGCCTGGTGCATGTTGAAGAG	652 AspGlyValTyraspAsnAlaGlu	2048 TTCCTAGAGGACATGGGCTTAAAGGCATTCACCAAAGTTCGTAAACCCAAAATG	1988 TATATTAATGGAATCACATATACTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC	1928 GÉCTTCCCTGGGCCTTTGAATGACCAGGACGATGAAGACTGCATCAATCGTCATAATGTC

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                                                                                          1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle 1034
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GlnLeuAsnValValTyrAsnVal 1246
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                                                                                                                                                               -----PrometAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCys 1238

    AGGACTGGGAAGGCTGCACAGGTGACTATCCAGTCTTCAGGG 3895

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Query Match:
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US-08-447-411-1
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                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
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Patent No. 5773243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:

CRASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/043,74

APPLICATION NUMBER: US 08/043,74

FILING DATE: 07-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5773243man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 1126-10

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: FRITZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BREDEHORST, REINHARD APPLICANT: BREDEHORST, REINHARD APPLICANT: VOGEL, CARL-WILHELM TITLE OF INVENTION: DNA ENCODING NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                       No.:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5211 base pairs
TYPE: nucleic acid
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CITY: Arlington
STATE: Virginia
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TELEX: 248855 OPAT UR
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120 GAAGAGCAAATTTTGGTGGAGGCCCATGGAGACAGTACTCCAAAATCGCTTGACATCTTT 179
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                                                                                                    21 AlaValAlaProGlyProArgPheLeuValThrAlaProGlyIleIleArgProGlyGly
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                                AsnValThrIleGlyValGluLeuLeu---GluHisCysProSerGlnValThrValLys
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                                                                     -TCCCACGGGCTCTCTATACCCTCATCACCCCTGCTGTTTTGCGAACAGACACA
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TyrIleGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGln	

939 LeuThrLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArg 958 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::	904 LeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCys 921	AspAsnArgLeuGlnSerThrLeuLysThrLeuSerPheSerPheProProAsn 88 GTAAAAGGAGTTGGTGGAACCAGGAACTTACGGTCATTAGATTAGATTAGATGACAAG 28 ThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAsp		792 IleLeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValPro 81	LeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeuGluIleThrIlePhe	SerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr::: ::: ACCTGG	2157 TGTTGTCACTACATCAAAGGGATCCGAGATGAAAACCAACGGGAGAGCGAGTTGTTTCTG 2216 674AsplleHisAspPheSerLeuGlySerSerProHisValArgLysHis 689 [
	Qy . 123 Db 397 Qy 125 Db 402 Ov 127	Qy 120 Db 385 Qy 122 Db 391	Qy 116 Db 373 Qy 118 Db 379	Qy 112 Db 363 Qy 114 Db 367	Qy 108 Db 353 Qy 110 Db 357	Qy 105 Db 342 Qy 106 Db 348	Qy 99 Db 324 Qy 101 Db 330 Qy 103
AACGTCGAATTGAACTT CysThrSerPheSerG1	1232 GlyPheGlyPheAlalleCysGlnLeuAsnValVyAsnValLysAlaSerGlySer 1251	7 Val' :::: 5 ATT' 0 Val' 5 GCT	68 LeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThrValAla 1187	128 GluSerLyBLeuSerABpSerTrpGlnProArgSerLeuABpIleGluValAlaAlaTyr 1147	108 ThrieuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla 1107	1054 ThrSerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAsp 1067 ::: 3420 ACTGCATTATTGGAATCCAGATCAGTCTGCAAAGAACAAATCAATATTCTAGACAGCAGC 3479 3420 ACTGCATTATTGGAATCCAGATCAGTCTGCAAAGAACAAATCAATATTCTAGACAGCAGC 3479 1068 ValGlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyr 1087 11:::::::::::::::::::::::::::::::::::	999 AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeu 1017

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RESULT 4
US-08-793-126-2
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 Percent Similarity:
                                     Alignment Scores: Pred. No.:
                                                                                       ; MOLECULE TYPE:
US-08-793-126-2
                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5056 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08793126 Patent No. 5849297 GENERAL INFORMATION:
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/793
FILING DATE: 07-FEB-1997
CLASSIPICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 1022
TELECOMMUNICATION INFORMATION:
TELECHIONE: (617) 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Harrison, Richard Alexander
APPLICANT: Farries, Charles Timothy
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Boston
STATE: MA
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CTGAGCCGGAAGGTACTGCTGGACGGGGTGCAGAACCCCCGAGCAGAAGACCTGGTGGGG 1012
                                 IleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMet 299
                                                                   ATTTCCCTGACTGAATCCCTCAAGCGCATTCCGATTGAGGATGGCTCGGGGGAGGTTGTG 952
                                                                                                                                                                                                                                                                                                                 PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGln-----ThrPro
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1835 GIGGLCGIGGALAAGGGGIGIICGIGCIGAAIAAGAACAAACIGACGCAGAGIAAG 1894 610 ValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer 629 :::	CCTGGGCAGCAGATGACCCTGAAGATAGAAGGTGACCACGGGGCCCGGGTGGTACTG ValalaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsn \	1742 GTAAAAGCGGCCAGTCAGAGAGACCGGCAGCCTGTA 1777 570 ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle 589		TTCATCCCTTCCGCCTGGTGGCGTACTACACGCTGATCGGTGCCAGCGGCCAGAGG GluIleIleSerAspValLeuLysIleProValGlnLeuVal	511 LysGINASnSerThrMetPheSerLeuThrProGluAsnSer 524 :::	491 LyBArgLeuLyBGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510	473ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn 490	HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr	AspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaVal:::::	LyslleAsnTyrThrValProGlnSerGlyThrPheLyslleGluPheProlleLeuGlu	ABNTYrThrGluTyrTrpSerGlySerABNSerGlyABNGlnLyBMetGluAlaValGln :::	GlnLeuThrLeuGluGluArgArgAsnAsnValValIleThrValThrGlnArg	LeuLysProSerLeuAsnPheThrAlaThrValLysValThrArgAlaAspGlyAsn	340 ThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePheAspTyrThrThrVal 359 :::	320 ProValGluIleLeuThrThrValThrGluSerValThrGlyIleSerArgAmnValSer 339	300 LysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerProGly 319
Qy 881 SerPheSerPheProProAsnThrValThrGlySerGluArg 894	863 SerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu	DD 2756 CTAAAGACCGGCCTGCAGGAAGTCAAGGCTGCTGCCGCAACGAACG	2696 CAGCAGACCATACCCCCCCAAGTCCTCGTTGTCCGTTCCATATGTCATCGTGCCG 825ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer	2648 CTCCACAATCCAGCCTTCTGCAGCCTGGCCACCAACCAAGAGGCGTCAC 805 GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro	2591 786	Qy 747 ProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeu 766	IleSerGluAspLeuGlyLeuGlyLeuThrThrThrProValGluLeuGlnAlaPheGln		Qy 697 TeuAspThrAsnMetGlyTyrArgIleTyr 706 Db 2375 GAGGACTTGAAAGAGCCCACCGAAAAATGGAATCTCTACGAAGCTC 2419	Qy 681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrp 696 :::	Qy 677AspPheSerLeu 680 ::: Db 2255 CGGCAGCACGCGGGGCCAGCCTGGGCCTGGCCAGGAGTAACCTGGATGAGGACATC 2314	Qy 667 GluAsnGluGlyHisILeValAspIleHis 676	Qy 652 AspGlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGlu 666 ::	Db 2075 ACGGAGAAGCGAATGGACAAAGTCGGCAAGTACCCCAAGGAGCTGCGCAAGTGCTGCGAG 2134	2015 CAGAGGGCAGAACTTCAGTGCCCGCAGCCAGCCGCCGGCCG	Qy 630 PheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAspAla 644 ::: Db 1955 GCCGGTGTCTTCTCCGACGCAGGGCTGACCTTCACGAGCAGTGGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC

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1205 IleGlnValThrValThrGlyProSerSer	1166 ArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThr 1185 ::: 3809 CGTTGGCTCAATGAACAGAGATACTACGGTGGTGGCTATGGCTCTACCCAGGCCACCTTC 3868 1186 ValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsn 1204 ::: ::: ::::::::::::::::::::::::	1130 LyBLeuserAspserirpGin	AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn	3503CAGGAGGCTAAAGATATTTGCGAGGAGCAGCAGCAGCAGCAGCAGCATCACT 3559 1074	GlupheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGly	987 TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006	950 LysGluLysAlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu 966	2984 AGAATTCTCCTGCAAGGGACCCCAGTGGCCCAGATGACAGAGGATGCCGTCGACGGAA 3043 911LeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPhe 929
PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/793,126 FILING DATE: 07-FEB-1997 ATTORNEY/AGENT INFORMATION: NAME: Baker, Hollie L. REGISTRATION NUMBER: 31,321	MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/132,271 FILING DATE: CLASSIFFCATON.	; CORRESPONDENCE ADDRESS: ; ADDRESSE: HALE AND DORR LLP ; STREET: 60 State Street ; CITY: Boston ; STATE: MA ; COUNTRY: United States of America ; ZIP: 02109 ; ZIP: 02109 ; COMPUTER READABLE FORM:	132-271-2. ence 2, Applient No. 622165 ERAL INFORMAT EPLICANT: Ha EPLICANT: FA ITLE OF INVEN	Db 4507 GGAAAGCTGTACCGGTTCTACCATCCGGAAAAGGAGGATGGAAAGCAAG 4561 Qy 1388 pLeuCysSerAspValGlnGlyCysArgProCysGluAsp 1401	SerGiuvalLysies SerGiuval	1302 nLeuLeuSerGlyPheMetValProSerGlu	nLysaspaspLeuAsnHisvalAspLe	

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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5056 base pairs
TYPE: nucleic acid
STRANDEDNESS:
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TOPOLOGY: lin
MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
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                                                                                                                                    GlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeu
                                                                                                                                                                                   ACGGTCATGGTCAACATTGAGAAACCCGGAAGGCATCCCGGTCAAGCAGGACTCCTTGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGG---AGTCCCATGTACTCTATCATCACCCCCAACATCTTGCGGCTGGAGAGCGAGGAG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACCACATGGGCAACGTCACCTTCACGATCCCAGCCAACAGGGAGTTCAAGTCAGAAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTCCCAGCCTGCTG------CTCCTGCTACTAACCCACCTCCCCCTGGCTCTG 112
PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGln-----ThrPro
|||:::||| ||||||||||| ::::::
                                                   GGCCAGTGGAAGATCCGAGCCTACTATGAAAACTCACCACAGCAGGTCTTCTCCACTGAG 712
                                                                                  GlyAspTrpSerIleGlnValGlnValAsnAsp------GlnThrTyrTyrGlnSer
                                                                                                                   TCTCAGAACCAGCTTGGCGTCTTGCCCTTGTCTTGGGAACATTCCGGAACTCGTCAACATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGCGCAACAAGTTCGTGACCGTGCAGGCC-----ACCTTCGGGACCCAAGTGGTG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeuAlaVal
                                                                                                                                                                                                                  SerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGln---TrpLeuSer
                                                                                                                                                                                                                                                     GGCTCCACAGTTCTCTATCGGATCTTCACCGTCAACCACAAGCTGCTACCCGTGGGCCGG 532
                                                                                                                                                                                                                                                                           LysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThr 162
                                                                                                                                                                                                                                                                                                                                    SerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysPro 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyr 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACTTCCCAGGCAAAAAACTAGTGCTGTCCAGTGAGAAGACTGTGCTGACCCCTGCCACC
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                                                                   1622 TTCATCCCTTCCTTCCGCCTGGTGGCGTACTACACGCTGATCGGTGCCAGCGGCCAGAGG 1681
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   GAGGTGGTCGACTCCGTGTGGGTGGACGTCAAGGACTCCTGCGTGGGCTCGCTGGTG
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                                                                                                                                   CGCCAGGTGCGAGAGCCCGGCCAGGACCTGGTGGTGCTGCCCCTGTCCATCACCACCGAC 1621
                                                                                                                                                                                                                                                                      CTCAGACCCGGGGAGACCCTCAACGTCAACTTCCTCCTGCGAATGGACCGCGCCCCACGAG 1501
                                                                                                                                                                                                                                                                                                                                                                     HisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLysThr------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLysMetGluAlaValGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTCCCTGCCTGAATCCCTCAAGCGCATTCCGATTGAGGATGGCTCGGGGGAGGTTGTG
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                                                                                                  TrpThrProLysAlaCysValIleValTyrTyr------IleGluAspAspGly
                                                                                                                                                                                                                                                                                                   -----ArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsn 490
                                                                                                                                                                                                                                                                                                                                        CCCTACAGCACCGTGGGCAACTCCAACAATTACCTGCATCTCTCAGTGCTACGTACAGAG 1441
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805 GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro 824 ::: ::: ::: ::: 2696 CAGCAGACCATAACCATCCCCCCAAGTCCTCGTTGTCCGTTCCATATGTCATCGTGCCG 2755	786LysSerAspLysPheAsplleLeuMetThrSerSerGluIleAsnAlaThrGlyHis 804 2648 CTCCACAATCCAGCCTTCTGCAGCCTGGCCACCACCACAAGAGGCGTCAC 2695	GluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGlu ::::: :::	ProPhePheIlePheLeuAsnLeuProTyrSerVall1eArgGlyGluGluPheAlaLeu 		GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal	GAGGACTTGAAAGAGCCACCGAAAAATGGAATTGGAATGGAAGCGTGTGGAAGCGTGTGGAAGAGCGGAAGGAGGAAGGGAAGGAA	GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrp	T::	GluAsnGluGlyHisIleValAspIleHis ::::::: GlyHisIleValAspIleHis	AspGlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGlu :::: GACGGCATGCGGGGAGAACCCCATGAGGTTCTCGTGCCACGCCCGGACCCGTTTCATCTCC	ACGGAGAAGCGAATGGACAAAGTCGGCAAGTACCCCAAGGAGGCTCCGCCAAGTGCTCCCAG	CAGAGGGCAGAACTTCAGTGCCCGCAGCCAGCCGCCCGACGCCGTTCCGTGCAGCTC	PhealaValPheGlnGluCysGlyLeuTzpValLeuThrAspAla	610 ValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer 629 :::		1742 GTAAAAAGCGGCCAGTCAGAAGACCGGCAGCCTGTA 1777 570 ProSerGluLysValSerLeuArgIleSerValThrGlnProAspSerIleValGlyIle 589	PheLysAsnLyslleLysLeuTyrTrpSerLysVa :::
Oy Cy	S & S	DB QY	Qy	dd VQ	β δ	Ag da	β Q	g &	B &	D Qy	D Qy	D Qy	B 64	Db Qy	Db Qy	Qy	D Qy
AAAGATAAGAACCGCTGGGAGGACCCTGGTAAGCAGCTCTACAACGTGGAGGCCACATCC TyralaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyTleProlleMet	1110 MetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpValSerSerGluSer 1129	AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn	1074PheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThrLeu 1089	1062 TyrGlnProAsnIleAspValGlnGluSerIleHis	1042 AsnLysSerProValThrLeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLys 1061 :::	1026 GluPheTrpAspProGlyArgValIleHisSerGluLeuGlnGlyGly	1007 GlnasnValLeuHisArgThrTyrThrTrpLeuLysGlyHisGlnLysSerAsnGly 1025	987 TrpLeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAsp 1006 ::: :::::::	967 TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr 986 :::::::::	950 LysGluLysAlaLeuSerPheMetArgGlnGlyTyrGlnArgGluLeuLeu 966	930 AlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysGlnLeuThrAspAsnLeu 949	911LeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPhe 929 	895ValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGly 910	881 SerPheSerPheProProAsnThrValThrGlySerGluArg 894	SerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeu ::::::	843 ABPAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGln 862 	825ThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSer 842

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RESULT 6
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                                                                                                                                                                     Sequence 23, Application Patent No. 6268485 GENERAL INFORMATION:
             APPLICANT: Farries, Timothy C.
APPLICANT: Harrison, Reichard A.
APPLICANT: Harrison, whichard A.
TITLE OF INVENTION: Down-Regulation Resistant
FILE REFERENCE: 4-30443/A/IMU/PCT
CURRENT APPLICATION NUMBER: US/09/142,334
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: PCT/GB97/00603
EARLIER FILING DATE: 1997-03-04
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OF SEQ ID NOS:
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TYPE: DNA
ORGANISM: Homo
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                 TTCTACTACATCTATAACGAGAAGGGCCTGGAGGTCACCATCACCGCCAGGTTCCTCTAC
                                       LeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyr
                                                                                           TTTGAGGTGAAGGAGTACGTGCTGCCCAGTTTCGAGGTCATAGTGGAGGCTACAGAGAAA
                                                                                                                   PheGlnValSerGluTyrValLeuProLysPheGluValThrLeuGln-----ThrPro
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Qy 825ThrHisbeuGLyGlülleProlleThrValThrAlabeuSerProThrAlaSer 842	805 GlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgPro	Qy 786LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHis 804 :::	Oy 767 GluileThrilePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGlu 785	Qy 747 ProPhePheIlePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeu 766	Qy 727 IleSerGluAspLeuGlyLeuGlyLeuThrThrProValGluLeuGlnAlaPheGln 746	Qy 707 GlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPheVal 726 ::::: :: Db 2431ATGAATATATTTTTGAAAGACTCCATCACCACGTGGGAGATTCTGGCTGTGAGC 2484	Qy 697 LeuAspThrAsnMetGlyTyrArgIleTyr 706 III	GlySerSerProHi8ValArgLys ::::: ATTGCAGAAGAGAACATCGTTTCCCGAAGT	Qy 677	667 GluAsnGlu	Qy 652 AspGlyValTyrAspAsnAlaGluTyrAlaGluArgPheMetGlu 666	Qy 645	Db 2026 CAGAGGGCAGAACTTCAGTGCCCGCAGCCAGCCGCCGACGCCGTTCCGTGCAGCTC 2085	630 PheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAspAla		390 VAIALAVALASPLYSSETVALASRLEUMECKSITA IASSETASPLIEINMEGGLUASN	1789 CCTC

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1090 AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn 1109 ::: :::	967 TyrGlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThr 986 ::::::::::::::::::::::::::::::::::::	2827 GACGGTGTCAGGAAGTCCCTGAAGGTCGTGCCGGAAGGAA
MESULT / US-08-662-227-1 US-08-662-227-1 US-08-662-227-1 ; Sequence 1, Application US/08662227 ; Patent No. 5922320 ; GENERAL INFORMATION: APPLICANT: WOGEL, CARL-WILHELM APPLICANT: WOGEL, REINHORST APPLICANT: BREDEHORST, REINHORST APPLICANT: FRITZINGER, DAVID TITLE OF INVENTION: RECOMBINANT PROCVF ; MUMBER OF SEQUENCES: 39 CCRRESPONDENCE ADDRESS: ADDRESSEE: P.C. ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY CITY: ARLINGTON STATE: VA COUNTRY: USA ZIP: 22202 COMPUTER READABLE FORM:	Db 1282 UASNVALCYSTRESSETLYPTOGIVARGSATGLEUMECGIUVALAS 1302	1186 ValalaLeuLysalaLeuSerGluPheAlaAlaLeuMetAsnThrGluArgThrAsn ::: ::::::: ::::

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-662-227-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 703-413-3000
TELEPAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5948 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILING DATE: 14-JUN-1996
CLASSIFICATION: 530
CLASSIFICATION: 530
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
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                               ValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSerIle---
                                                                                 TTTCAGACTCCAGAAGGCATTCTTGTCAGT-----
                                                                                                                                                                                                                                                                                                                        CAAGTAACTGGTCCTCAAGTGAGATTGGAAAAGGTGGTTCTCTTTTCTTACCAGAGTAGC
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                                                                                                                                                           TATCGTGTTTTTTCTATGGATCACAACACAAGAAGATGAACAAAACTGTGATTGTTGAG
                                                                                                                                                                                                PheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIleLeu 167
                                                                                                                                                                                                                                                                        ArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluValLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAAACCAGAGTAGATATGAATCCAGCAGGAGGCATGCTTGTCACT-----CCAACT 261
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TTCTTC---TGGCCTTACAATTTACCAGACCTTGTCAGTTTGGGGGACTTGGAGGATTGTG
                                                                                                                     IleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAspLeuGly 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTCCAAAACCACTTGACATCTTTGTTCATGATTTTTCCACGGAAGCAGAAAACCTTGTTC 210
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                                                                                                                                                                                                                                        ----TTTCTGTTTATCCAGACAGATAAAGGCATCTATACACCAGGGTCTCCAGTACTC
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                                                                                                                                                                             LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLys---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCCTGAACATACCATTGAATGCTCAA-----AGCCTACCAATCACTGTTAGAACT 1248
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                  CCTTCCTTCCGGTTTGTGGCTTACTACCAAGTGGGAAACAACGAAATTGTGGCTGATTCT 1608
                                                    ProLysAlaCysValIleValTyrTyrIleGluAspAspGlyGluIleIleSerAspVal 546
                                                                                                                                      -----GlnAsnSerThrMetPheSerLeuThrProGluAsnSerTrpThr 526
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RESULT 8
US-09-017-947-1
Sequence 1, Application US/09017947
. Patent No. 6303754
GENERAL INFORMATION:
APPLICANT: WOGEL, CARL-WILHELM
APPLICANT: BREDEHORST, REINHORS:
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                                                                                                                                                                                                                                                                                                                                                                                  CysArgProCysGluAspGlyAlaSerGlySerHisHis----
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  VOGEL, CARL-WILHELM BREDEHORST, REINHORST
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Query Match:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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                                       GlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThrLys 127
                                                                               ATAGAGATTCCAGCAAAAGAAGTGAGTACGGACTCCAGGCAAAATCAATATGTGGTTGTG 321
                                                                                                                                                                                                                                                                                                                                                                                  ProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeu---GluHis 51
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                                                                                                                         LeuThrLeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgValThr 107
                                                                                                                                                                                                             AsnLeuThrValSerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThr 87
                                                                                                                                                                                                                                                      ACTCCAAAACAGCTTGACATCTTTGTTCATGATTTTCCACGGAAGCAGAAAACCTTGTTC
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Matches:
Conservative:
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226 LeuProLysBheGluValThrLeuGlnThrProLeuTycCysSerMethan 242 [ArgileServalPheileGlnThrAspLysAlaLeuTyrLysProLysGlnGluValLys ::
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1069 GlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr 1088	1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspVal 1068 ::: :::: 3400 GCGTTGTTGGAATCCAAAACAATCTGCAATGACTATGTCAATAGTCTAGACAGCAGCATC 3459	1038 LeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054 ::: ::: 3340 ATGCAGGGAAGTATTCAAGGTGCTGAAGAAGAAGTATATTTAACAGCTTTCATTCTGGTT 3399	1018 LysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGlu 1037	999 AlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTrpLeu 1017	980 TyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArgCysPheLeuGlu 998 ::: ::: ::: :::: ::: 3166CGTGCATCTAGTTCTTGGCTAACAGCATATGTCGTAAAAGTCTTTGCCATGGCT 3219	960 GlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAlaPheGlyAsn 979	940 ThrLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGln 959 ::: ::	923 GluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeu 939 	905 GlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCysGly 922	885 ProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeu 904	871 AsnArgLeuGlnSerThrLeuLysThrLeuSerPheSerPhe 884 :::	851 VallysAlaGluGlyIleGluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAsp 870	831 ProIleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeu 850 	813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIle 830	793 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812	773 TyrLeuLyBAspAlaThrGluValLyBValIlleIleGluLyBSerAbpLyBPheAspIle 792 ::: ::: ::: 2518 TACGTTAACGAGGATATTTATGTGCGAGTGGAACTGTTATACAACCCAGCCTTC 2571	753 AsnLeuProTyrSerVallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsn 772 ::: ::::: :::: 2458 CAAATGCCATATTCAGTAGTGAAGAATGAGCAGGTGGAGATTCGAGCTATTCTGCACAAC 2517	::: :::::: :::
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Best Local Similarity:
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                                Query Match:
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                                                                                                                     Alignment Scores:
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TELEPHONE: (703) 413-2020
TELEPAX: (703) 413-2220
TELEX: 240855 OPAT UR
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 5924 base pairs
TYPE: nucleic acid
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Patent No. 57
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APPLICANT: FRITZI
APPLICANT: BREDEH
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NAME/KEY:
LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                    FEATURE:
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MEDIUM TYPE: Floppy
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CITY: Arlington
STATE: Virginia
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REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                               AspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIle-----
                                                                                                                                                                      MetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSerSerPro
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Db 2986 ĠAĠCAÁAĀTĀTĠĀTĊCGCATGĠĊĊGCACCAĞTTATTGCCACCTĀĊTACCTĠĠĀĊACCACA 3045 Qy 940 ThrLysGlpsLysGlpLeuThrAspAspLeuLysGluLysAlaLeuSerPheMetArgGln 959	Db 2866 CCTGACACAGAAATTGAAACCAAGATTATCATCCAAGGTGACCCTGTGGCTCAGATTATT 2925 Qy 905 GlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCysGly 922 ::	871 AsnArgLeuGlnSerThrLeuLysThrLeuSerPheSerPhe :::		793 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer	Qy 753 ABDLeuProTyrSerVallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsn 772	Qy 713 ValProAspSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGly 732 :::	TCAAGDTNIABMETGILTTCCCCAAGAGTTGGTTGTGGCTAACAAGDTNIABMETGJYTYTATGILGTYTGJUPAGILVAJTHY AAGGACTTGACCGAGGAGCCTAACAGGGATTTCAAGCAAG	2122 662 2182	Qy 649 649 Db 2062 ATGGGGTACACTTGTGAAAAGCGTGCAAAATACATCCAGGAGGGAG

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1253 ATGATGATGATGATGATGATGATGATGATGATGATGATGA	ThrValThrGlyProSerSerProSerProLeu	1149 LeuLeuSerHisPheLeuGlnPheGlnThrSorGluGlyIleProIleMetArgTrpLeu 1168	1069 GlnGluSerTleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr 1088 :::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::
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FOR SEQ ID N	X: (703) 413-2220 248855 OPAT UR		REFERENCE/DOCKET NUMBER: 1126-101-0	NUMBER: 24,618	INFORMATION:	0/010,/1	A:	-		CATION DATA:	PatentIn Release	SYSTEM: PC-DC	TIPE: PLOOPY CIEK	READABLE FORM:	22202	Y: U.S.A.	Virginia	: 1755 S. Jefferson Davis Highway, Suite 400	: P.C.	ADDRESS:	ENCES: 81	Ę	T: BREDEHORST, REINHARD	FRITZINGER,	INFORMATION:	;, Application US/08447411	-75	CGAATAGAAGAA 4602		TyrpheMetGlu 1425	TTACAAATTGAAAAAGCCTGCGAGACGAATGTGGATTATGTCTACAAAACCAAGCTGCTT	rSerValllePhellePheCysPheLysLeuLeu	TGCCGATGTGCAGGAAAACCTGTTCCTCGCTCAACCATCAGGAAAGGATTGATGTTCCA		AAGTTCTACCATCCAGATAAAGGAACAGGCCTTCTCAATAAGATATGTATTGGTAACGTT	gSerTyrAsnSerGluValLysLeuSerSerCysAspLeuCysSerAspValGlnGly	TGTACAGCTACTACAATCTAGATGAAAAATGTACC	AsnThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGlnAlaVal	GTCTCCCACTCTGAAGATGAATGCCTGCACTTTAAGATTCTCAAGCATTTTGAAGTTGGC		ATATGAAGTTGACAATAATATGGCTCAGAAAGTAGCTGTTATCATTTACTTAAACAAG		TTTCTCCCTGATGCTGAAGACCTTACAAGGCTTTCTAAAGGAGTGGACAGATACATCTCC 4	GluAlaIleSerLeuSerGluThrValLys	${\tt AGGTATCTGGGAGAAGTTGATTCTACAATGACAATAATTGATATTTCTATGCTGACTGGT}$
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LENGTH: 4138 base pairs
TYPE: nucleic acid
STRANDEDMESS: unknown
TOPOLOGY: unknown
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                                                                                                                                                                                                                                                                                                                   ArgGlyGlnLeuValAlaValGlyLysGlnAsnSer----
                                                                                                                                                                                                                                                                                                                                                        GTGAGGGGCAATGCAAATTCACTGAACCAGATCÁAATATTTCACATÁCCTCATACTGAAT 494
                                                                                                                                                                                                                                                                                                                                                                                  ValSerGlyAsn------LysArgLeuLysGluLeuSerTyrMetValValSer 502
                                                                                                                                                                                                                                                                                                                                                                                                                        CATGTAGCCATTACATCTACAGAGATTAAGCCCGGAGATAACTTACCTGTCAATTTCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAATAAAGTCCATGACAGCCACAGCCTACCAAACCCAGGGAGGATCTGGAAACTATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlySerLysSerSerMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIle
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                                              TrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGln 582
                                                                                                                                                                                                                    ATGAATCTACATATCACTCCAGAT----CTCATTCCTTCCGGTTTGTGGCTTAC
                                                                                                                                                                                                                                                     Met---PheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleValTyr
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                                                                                                                                                   TyrileGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGln-----
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768.50
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                   ----CCAGGAGCTGCAATGAAAATCAAATTGGAA----GGGGAT 761
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851 ValLysAlaGluGlyIleGluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAsp 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThr
                                                                                                                         GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGly-----GluIle
                                                                                                                                                                     GCTTCCACAGAAAGTCAA---
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                                                                ProIleThrValThrAlaLeuSerProThrAlaSerAspAlaValThrGlnMetIleLeu
                                                                                                   CTGTCCTCCAGGGCAGTATCGTTTGTGATAGTCCCATTAGAGCAAGGATTGCATGATGTT
                                                                                                                                                                                                 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812
                                                                                                                                                                                                                                   TACGCTGACAAGGATATTTATGTACGAGTGGAACTGTTATACAGCCCAGCCTTCTGCAGT 1625
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                                                                                                                                                                                                                                                                 TyrLeuLysAspAlaThrGluValLysValIleIleGluLysSerAspLysPheAspIle
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                                                                                                                                                                                                                                                                                                                                                                                                   -ProValGluLeuGlnAlaPheGlnProPhePheIlePheLeu
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	eProIleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSerThrGl 1182	eGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyII 1162 ::: ::: TGAAGGCACTTCCTATGCCTTGTTGGCCCTGCTGAAAATGAAGAAATTTGTTGAGGCCGG 2743	nPheTrpValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspII 1142	LysGluAlaLeuAsn-MetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGl 1122	AspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAla 1104	LeuGluSerGluPheSerArgGly		ysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIleHisSerGlu 		99.8	979 221		pTyrLeu 939	lyproSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCysGly :::	ProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeu 904	AsnArgLeuGlnSerThrLeuLysThrLeuSerPheSerPhe 884 :::	
TYPE: F1 ER: IBM F ING SYSTEM	COUNTRY: USA ZIP: 22202 COMPUTER READABLE FORM:	SEE: P.C. : 1755 S. JEFFERSON DAVIS HIGHWAY ARLINGTON	TITLE OF INVENTION: RECOMBINANT PROCVE INTER OF SEQUENCES: 39 CORRESPONDENCE ADDRESS: ADDRESSE: OBLON SPIVAK, MCCLEILAND, MAIER & NEUSTADT,	E E E E	WESOLF 11 US-08-662-227-33 ; Sequence 33, Application US/08662227 ; Patent No. 592230 ; Patent No. 592230 . GENERAL INCOMMATION.	Qy 1388 pLeuCysSerAspValGlnGlyCysAxgProCysGluAspGlyAlaSer 1404	Qy 1368 rGluProArgArgGlnAlaValArgSerTyrAsnSerGluValLysLeuSerSerCysAs 1388		Qy 1318 uThrValLysLysValGluTyrAspHisGlyLy 1329	Qy 1299 tGluValAsnLeuLeuSerGlyPheMetValProSerGluAlaIleSerLeuSerGl 1318 :::: ::::: :::: :::: :::: ::::	Qy 1279 sValAspLeuAsnValCysThrSerPheSerGlyProGlyArgSerGlyMetAlaLeuMe 1299	Qy 1266 uAspValAlaValLysGluAsnLysAspAspLeuAsnHi 1279	Qy 1246 lLysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGluAlaPheAspLe 1266 ::: :::	Qy 1228IleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnVa 1246	Oy 1218 1227 Oy 1218 1227 DD 2924 AATTAATTATGAAAATGCTCTCCTGGCTCAGACAGTAGAGACCAAACTCAACGAAGACTT 2983	GGACTTAAACTTAGATATTACTATTGAACTGCCAGATCGAGAAGTACCTATAAGGTACAG	2804 AGCAACAGTTATGATGTTTCAAGCTCTTGCTGAATATGAGATTCAGATGCCTACCCATA

Qy 535 TyrileGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGln 552	Qy 516 MetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleValTyr 534	Qy 503 ArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThr 515 ::: :::::: :::: ::: :::: :::: :::: :::: ::::	Qy 487 ValSerGlyAsnLysArgLeuLysGluLeuSerTyrMetValValSer 502	Qy 469 GlnLeuLysThrArgAspGluAsnIleLysValGlySerProPheGluLeuVal 486 ::: Db 375 CATGTAGCCATTACATCTACAGAGATTAAGCCCGGAGATAACTTACCTGTCAATTTCAAT 434	QY 449 GlySerLysSerSerMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIle 468	QY 429 LysileGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeu 448	Qy 409 AsnGlnLysMetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe 428 ::: :::	Qy 389 ValValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGly 408	Oy 369 ThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsn 388	QY 349 TyrileileGluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAla 368	US-10-020-095-4 (1-1428) x US-08-662-227-33 (1-4138)	10.46% Indels: 2 Gaps:	Pred. No.: 6.68e-71 Length: 4138 Score: 768.50 Matches: 306 Percent Similarity: 41.88% Conservative: 212	ULE TYPE: 227-33 Scores:	; LENGTH: 4138 base pairs ; TYPE: nucleic acid ; STRANDEDNESS: single ; TOPOLOGY: linear	; TELEPHONE: 703-413-3000 ; TELEFAX: 703-413-2220 ; INFORMATION FOR SEQ ID NO: 33: ; SEQUENCE CHARACTERISTICS:	2000	; FILING DATE: 14-JUN-1996 ; CLASSIFICATION: 530 ; ATTORNEY/AGENT INFORMATION:	; SOFTWARE: PatentIn Release #1.0, Version #1.30; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/662,227
B &	da A	5 B &	g &	Q dd Q	Db QY	Qy Db	9d \$	5 B &	S B &	Db	Db	, 85	Qy dd	QV	B &	dg Qy	B &	Db	ο Β
793 LeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812	1366 TACGCTGACAAGGATATTTATGTACGAGTGGAACTGTTATACAGCCCAGCCTTCTGCAGT 1625	ASILENTOTYTSETVALLIENIGSTYCHUSINFREALALEUGINITERINITIEPREASH	GGGATCTGTGTGGCTGAACCTTATGAAATAACAGTCATGAAAGACTTCTTCATTGAATCTT	TrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThrThr	700 AssMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSer 719 :::		1242 GCAAGAAGTGATTTTGAAGATGATTTATTTGGAGAAGGTAACATCACCTCAAGGTCT 1298	TGCTGTCACTACATCAAAGGGATCCAAGATGACAATAAACGGGAGAGCGAGTTGTTTCTG	AlaGluTyrAlaGluArgPheMetGluGluAsnGluGly	648	1002 AGGCGTCGCAGTTCTGTTTTGCTGCTTGACAGCAACGCAAGCAA		643 AspAlaAsnLeuThr 647 942 AGCACTAATCTCAACACCCAAACAGGATCAGCTGCAAAGTGTCCTCAGCCTGCAAATCGG 1001	623 LeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThr 642	603 ASDASpIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThrGlyTyrTyr 622	583 ProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSer 602	563 TrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerValThrGln 582	TGCATGGGAACGTTGGTTGTGAAAGGAGGACGACTTCCAGAGACAATCGAATACAAATG	609 TACCAAGTGGGAAACAATGAAATTGTGGCTGATTCTGTCTG

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AspAsnTyrThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAla 1104	QAGGITACAGCAAGTGCAGGAGAGTTGATGTCAGATGAAGAAAACTGAAA 1793 VallyshlaGluGlyIleGluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAsp 870	GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIle 830
US-09-017-947-33 ; Sequence 33, Application US/09017947 ; Patent No. 6303754 ; Patent No. 6303754 ; Patent No. 6303754 ; APPLICANT: WOGEL, CARL-WILHELM APPLICANT: BREDEHORST, REINHORST APPLICANT: KOCK, MICHAEL APPLICANT: KOCK, MICHAEL APPLICANT: REITZINGER, DAVID TITLE OF INVENTION: RECOMBINANT PROCVF NUMBER OF SEQUENCES: 39 ; CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,	The paptheth valial aleuly shi aleu Sergiu Pheal a Aleu Met As Through a Concocart Tragatity Pheal and the West As Through As Concocart Tragatity Pheal and the West As Through Proser For Proser Fo	Qy 1142 eGluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSerGluGlyI1 1162

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Qy 429 LysIleGluPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeu 448	Oy 389 ValValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGly 408	YEIleIleGluphePheAspTyrThrThi 	Alignment Scores: 6.68e-71 Length: 4138 Pred. No.: 768.50 Matches: 306 Score: 768.50 Matches: 306 Percent Similarity: 41.88* Conservative: 212 Best Local Similarity: 24.74* Mismatches: 465 Query Match: 10.46* Indels: 255 DB: Gaps: 46 US-10-020-095-4 (1-1428) x US-09-017-947-33 (1-4138)	TELEPHONE: 703-413-3000 TELEPAX: 703-413-2220 INFORMATION FOR SEQ ID NO: 33: SEQUENCE CHARACTERISTICS: LENGTH: 4138 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA US-09-017-947-33	; FILING DATE: ; CLASSIFICATION: ; PRIOR APPLICATION DATA: ; PRIOR APPLICATION NUMBER: US 08/662,227 ; FILING DATE: 14-UN-1996 ; ATTORNEY/AGENT INFORMATION: ; NAME: OBLON, NORMAN F. ; REGISTRATION NUMBER: 24,618 ; REFERENCE/DOCKET NUMBER: 1126-0107-0X ; TELECOMMUNICATION INFORMATION:	ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY CITY: ARLINGTON STATE: VA COUNTRY: USA ZIP: 22202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/017,947
Qy 689 HisPheProGluThTTpII=TxpLeu	1182 TGCTGTCACTACATCAAAGGGATCCAAGATGACAATAAACGGGAGAGCGAGTTGTTTCTG 678	648LysAspTyrIleAspGlyValTyrAspAsn 1062 GATCAAGACCTGCGTAAATGCTGTGAAGATGGCATGAGAACCCCATGGGGCACACT 658 AlaGluTyrAlaGluArgheMetGluGluAsnGluGly	643 ASDALABRILEUThr	Qy 583 ProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSer 602	Db 609 TACCAAGTGGGAAACAATĠAÀÁTTGTGGCTĠÁTTCTGTCTGGGTGGATĠTGAAGGATACC 668 Qy 553LeuValPheLys	Db 435 GTGAGGGGCAATTCACTGAACCAGATCAAATATTTCACATACCTCATACTGAAT 494 Qy 503 ArgGlyGlnLeuValAlaValGlyLysGlnAsnSerThr 515

683 -SerProHisValArgLysHisPheProGluThrTrpIleTrpLeuAspTh	668 nGluGlyHisIleValAspIleHisAspPheSerLeuGlySer	657ABRALAGLUTYRALAGLUATGPheMetGluGluAs 668		GCAAGTCGGGTTCAAACACCCTGTTTTCAAAACTCCCCAACTCTGCCTCTGGTCTGC	-GluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSer 		AspLysSerValAsnLeuwetAsnAlaSerAsnAspIleThrMetGluAsnValValla	572 uLysValSerLeuArgileSerValThrGlnProAspSerIleValGlyIleValAlaVa 592	IPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGl	534 rTyrileGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGlnLeuVa 554	514 rThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysValIleValTy 534	### ##################################	483PheGluLeuValValSerGlyAsnLysArgLeuLy 494 ::::: 16483 GGATGCTCAGGAGTTGTATCTGTTCTACGACCTGACCTCAGGCAGG	ulysthrärgaspGluasnllelysValGlySerPro	rMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIleGlnLe TCAGTTGTCGAATCCCTCCCAAGGCCTTTGGACATATGTGGCGGA	435 uGluaspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSe 453 GluaspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSe 453	425SerGlyThrPheLysIleGluPheProIleLe 435	416
Qy 1016 p	Qy 996 eLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyrThrTr 1016 :	CTCGCTTTACAAAAATCGCCCTTGTCCTCGGACGAATTGCCTTGGCGCGCGGAGATGCTG	975 rAlaPheGlyAsnTyrAspProSerGlySerThrTrpLeuSerAlaPheVal		Qy 939 uThrlysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSe 955	Qy 919 rGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrIe 939	Qy 899 alleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTy 919	Qy 879 rLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGlnIleThrAl 899 ::: ::: Db 15238 GATTCTCTACGGCGGACAGTCCCAAACGGTG15208	rTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysTh	Qy 839 oThrAlaSerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIleGluLysSe 859	uPheProlleArgProThrHisLeuGlyGluIleProIleThrValThrAlaLeuSerPr	799 eAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLe			Qy 739 oValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerValI1 759	Qy 719 rTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThrThrPr 739	Qy 699 rAmmetGlyTyrArgileTyrGlnGlupheGluValThrValProAmbberileThrSe 719	AGAATCCTCCGTGCGTACCAATTTCGCTGAGACTGCATTCTTTGAGCCGGCATTGCTGAC

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Sequence 3, Application US/09241606
Patent NO. 6472140
GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Kovacs, Dora
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin
TITLE OF INVENTION: Alzheimer's Disease
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SEQ ID NO 1
LENGTH: 339
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APPLICANT: Gonias, Steven L.
TITLE OF INVENTION: Transforming Growth Fa
FILE REFERENCE: 00370-02
CURRENT APPLICATION NUMBER: US/09/311,352B
CURRENT FILING DATE: 1999-05-13
NUMBER OF SEQ ID NOS: 6
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                                                                                                                                                                                                             SerVallleArgGlyGluGluPheAlaLeuGlu 767
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SEQ ID NO 3
LENGTH: 750
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CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
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NAME/KEY: CDS
LOCATION: (1)...(750)
OTHER INFORMATION: A /LRP Binding
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ORGANISM: Homo sapiens
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                                               ThrGlnAspAlaSerValSerIleValAspTyrTyrGluProArgArgGlnAlaValArg 1376
                                                                                                                                                                                                                      GATGTGAAGATGGTCTCTGGCCTTCATTCCCCCTGAAGCCAACAGTGAAAAATGCTTGAAAGA 531
                                                                                                                                                                                                                                                                                      CAAATCTCCCTAAGTGTCAGTTACACAGGGAGCCGCTCTGCCTCCAACATGGCGATCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCATGAAAGTGACAGGAGAAGGATGTGTCTACCTCCAGACCTCCTTGAAATACAATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCGTGAAGTGGATCACGAAGCAGCAGAATGCCCCAGGGCGGTTTCTCCTCCACCCAGGAC
                                                                                                                 ValAsnGluThrGlnPheCysValAsnIleProAlaValArgAsnPheLysValSerAsn 1356
                                                                                                                                                                                 SerGluThrValLysLysValGluTyrAspHisGlyLysLeuAsnLeuTyrLeuAspSer
                                                                                                                                                                                                                                                                                                                        AsnValCysThrSerPheSerGlyProGly-----ArgSerGlyMetAlaLeuMet 1299
                                                                                                                                                                                                                                                                                                                                                           GCTTTAGGAGTGCAGACTCTGCCTCAAACTTGTGATGAACCCAAAGCCCACACCAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                           AspValAlaValLys-----GluAsnLysAspAspLeuAsn---HisValAspLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACAACAACCATCGCCTGTTACTGCAGCAGGTCTCATTGCCAGAGCTGCCTGGGGAATAC
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Matches:
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Qy 1377 SerTyrAsnSer 1380
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Db 712 GAGTACAATGCT 723

Search completed: January 17, 2004, 01:18:53
Job time: 445 secs

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Result
No.
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Maximum DB seq length: 2000000000
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-Qsqn2 1/USPTO spool p/US1002095/runat 15012004 163824 18739/app query.fasta_1.1607
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -WATRIX=blosum62
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-NCPU=6 -TCPU=3 -NO MMAP -LARGSQUERY -NGE SCORES=0 -WAIT -DSPBLOCK=100 -
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Command_line parameters:
                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
           Score
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Query
Match Length DB
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Listing first 45 summaries
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/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq;*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq;*
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/cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq;*
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/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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                                                                                           SUMMARIES
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5, Appl 2, Appl 172, Appl 172, Appl 173, Ap 1531, Ap 266, Ap 270, Ap 270, Ap 270, Ap 270, Appl 270	181 953 7, 7 1, 7 223 3, 7 19, 7 178

ALIGNMENTS

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RESULT 1

US-09-833-381-1810

Sequence 1810, Application US/0983381

Patent NO. US20020132090A1

GENERAL INFORMATION:
APPLICANT: Robison, Keith E.

TITLE OF INVENTION: No. US20020132090A1el Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/833,381

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 09/516,448

PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOSTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 1810

LENGTH: 3033

TYPE: DNA

ORGANISM: Homo sapiens

US-09-833-381-1810

Alignment Scores:
Pred. No.:
4535.50

Matches:
B80

Conservative: 2
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866 LeuAspLeuThrAspAsnArgLeuGlnSerThrLeuLysThrLeuSerPheSerPhePro 885 	846 ThrGlnMetIleLeuValLyBAlaGluGlyIleGluLyBSerTyrSerGlnSerIleLeu 865 	826 HisLeuGlyGluIleProIleThrValThrAlaLeuSerProThrAlaSerAspAlaVal 845 	806 GlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIleArgProThr 825 	786 LysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHisGln 805 	766 LeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysValIleIleGlu 785 	746 GlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArgGlyGluGluPheAla 765 	726 ValileSerGluAspLeuGlyLeuGlyLeuThrThrProValGluLeuGlnAlaPhe 745	706 TyrGlnGluPheGluValThrValProAspSerIleThrSerTrpValAlaThrGlyPhe 725 	686 ValargLysHisPheProGluThrTrpIleTrpLeuAspThrAsnMetGlyTyrArgile 705 	666 GluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeuGlySerSerProHis 685	646 LeuThrLysAspTyrIleAspGlyValTyrAspAsnAlaGluTyrAlaGluArgPheMet 665 	626 PheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsn 645 	606 ThrmetGluAsnVallvalHisGluLeuGluLeuTyrAsnThrGlyTyrTyrLeuGlyMet 625	586 IleValGlyIleValAlaValAspLysSerValAsnLeuMetAsnAlaSerAsnAspIle 605 	566 VallysAlaGluProSerGluLysValSerLeuArgIleSerValThrGlnProAspSer 585 	546 ValleutysIleProValGlnLeuValPhetysAsnLysIleLysLeuTyrTrpSerLys 565	-4 (1-1428) x US-09-833-381-1810 (1-3033)	Best Local Similarity: 97.78% Mismatches: 1 Query Match: 61.72% Indels: 17 DB: 10 Gaps: 1
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RESULT 2
US-10-108-260A-953
; Sequence 953, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full
; FILE REFERENCE: H1-A0106
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Score:
                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 953
SEQ ID NO 953
TYPE: DNA
ORGANISM: Homo sapiens
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                                          MetGlnGlyProProLeuLeuThrAlaAlaHisLeuLeuCysValCysThrAlaAlaLeu
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Sequence 7, Application US/10292081A
Publication No. US20030162202A1
GENERAL INFORMATION:
APPLICANT: Kenneth David Becker
APPLICANT: Gonul Velicelebi
APPLICANT: Xin Wang
APPLICANT: Randolph E. Tanzi
APPLICANT: Lars Bertram
APPLICANT: Aleister J. Saunders
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APPLICANT: LARS BETTRAM
APPLICANT: Aleister J. Saunders
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 37481-3323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/337434
PRIOR APPLICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                      GTGGCCTCAAGCAATTTTCCTTTTTCCCCTCTCATCAGAGCCCTTCCCAGGGCTCCTACAAG
                                                                                                                                                                                                                                                                                                            LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer
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                                  GTGACTGTGAGCATTTGCAGAAAGTATAGTGACGCTTCCGACTGCCACGGTGAAGATTCA
                                                               ValThrLeuThrPheLeuProLeu-
                                                                                               GAAGAGATGAATGTATCAGTGTGGCCTATACACATATGGGAAGCCTGTCCCTGGACAT
                                                                                                                                                           TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA
                                                                                                                                                                                                                           GTGGTGGTACAGAAGAAATCAGGTGGAAGGACAGAGCAC---CCTTTCACCGTGGAGGAA
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	S61 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580	541 GluileIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560	21 ProGluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGly 540 1630 GTGAAGTCAGACATTGCTCCTGTCGCTCGGTTGCTCATCTATGCTTACCGGG 1689	511	493 LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510 :::	479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492	459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478	439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458	429 LysileGluPhePro	412 MetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe 428	392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411 :::	372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValIle 391	352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371	332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316	277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296	892 CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA 951
877 LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln 896 :::			ThrValThrAlaLeuSer	GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle		ThrGluValILysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer	ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAenTyrLeuLysAspAla				GlySerSerProHisValArgLyBHisPheProGluThrTrpIleTrpLeu	AlaGluA GAGTCAG	10 As	ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle ::::::::::::::::::::::::::::::::::::	TyrasnThrGlyTyrTyrLeuGlyMetPheMetAsnSerPheAla	GGCTTCCCTGGGCCTTTGAATGACCAGGACAATGAAGACTGCATCAATCGTCATAATGTC		GCTCCTCAGTCCGTCCCTCCGTGCTGGACCAAAGCGTGCTGCTCATGAAG

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                                                                         SerProLeuAlaValGln-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGlyIlePro------IleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175
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ACATTTTCCAGCAAATTCCAAGTGGACAACAACCGCCTGTTACTGCAGCAGGTCTCA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGGACCTGACCTCTGCAACCAACCATCGTGAAGTGGATCACGAAGCAGCAGAATGCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAsnMetLeuThrTrpArgAlaGluGluGluGlyGlyMetGlnPheTrp------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCAAGTCACTTAATGAGGAAGCTGTGAAGAAAGACAACTCTGTCCATTGGGAGCGCCCCT 3600
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                                                                                                                                                        AGGACTGGGAAGGCTGCACAGGTGACTATCCAGTCTTCAGGG 3894
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5 밁 Ś 밁 5 문 δ 밁 Ş 밁 S 밁 8 밁 S 닭 8 맑 δ 8 Ś 밁 5 밁 Ś 뫄 Ś 밁 δ В δ 밁 δ 밁

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; NAME/KEY: sig peptide
; LOCATION: (44)..(112)
; NAME/KEY: CDS
; LOCATION: (44)..(4468)
; NAME/KEY: mat_peptide
; LOCATION: (113)..(4468)
US-10-052-817-1
                                                                                                                                                                                                                                                                                                                                APPLICANT: Saunders, Aleister J.

TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and TITLE OF INVENTION NUMBER: US/10/052,817

CURRENT FILING DATE: 2002-01-23

PRIOR APPLICATION NUMBER: 09/241,606

PRIOR FILING DATE: 1999-02-02

PRIOR APPLICATION NUMBER: 09/148,503

PRIOR TILING DATE: 1998-09-04

PRIOR APPLICATION NUMBER: 06/093,297

PRIOR APPLICATION NUMBER: 60/093,297

PRIOR APPLICATION NUMBER: 50/093,297

PRIOR APPLICATION NUMBER: 50/093,297

PRIOR APPLICATION NUMBER: 50/093,297

PRIOR PILING DATE: 1998-07-17

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIN Ver. 2.0
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US-10-052-817-1
; Sequence 1, Application US/10052817
; Publication No. US20020114792A1
; GENERAL INFORMATION:
                  Alignment Scores: Pred. No.:
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                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                LENGTH: 4577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATGTCTTGATTTACCTTGATAAGGTGTCAAATCAGACACTGAGCTTGTTCTTCACGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCAACAGTGAAAATGCTTGAAAGATCTAACCATGTGAGCCGGACAGAAGTCAGCAGCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GluAlaIleSerLeu-----SerGluThrValLysLysValGluTyrAspHisGly 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer 1311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGACGGATGAGTTTGCAATTGCTGAGTACAATGCT 4437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCAAGATGTCCCAĠŤÁAGAGATCTGAAACCAĠĊĊATAĠŤĠAAAGTCTATĠÁŤŤÁČŤÁĊ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348
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2.83e-133
1441.00
Length:
Matches:
4577
451
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for

Qy 297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316	Oy 277 LysLysAsnileThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296	Qy 272SerPheTrpGlyLy8 276	Qy 264 ValThrLeuThrPheLeuProLeu	Oy 244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::::::::::::::::::::::::::::::::::::	Qy 224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 ::: 113 TTTGTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA 772	Qy 206 IleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223 :::	QY 186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205 :::	Qy 167 LeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185 ::: :::	Oy 147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166	Oy 127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 146 ::: ::: ::::	Oy 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126	Qy 90 LeuProSerLeuProLeuAsnSerAlaAspGlulleTyrGluLeuArgVal 106 :::::: ::: Db 311GCTGTCCCAAAGTCTTCATCCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG 364	Qy 72SerValLeuGluAlaGluGlyValPheGluLy8GlySerPheLy8ThrLeuThr 89 ::: Db 263 TTCACTGACCTGGAGGGCGGAGAATGACGTACTCCACTGTGTCGCCTTC 310	203 CTGAATGAGACAGTGACTGTAAGTGCTTCCTTGGAGTCTGTCAGGGGAAACAGGAGCCTC	52 CysProSerGlnValThrValLy	Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51	Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31	US-10-020-095-4 (1-1428) x US-10-052-817-1 (1-4577)	Percent Similarity: 46.20% Conservative: 266 Best Local Similarity: 29.06% Mismatches: 551 Query Match: 19.61% Indels: 284 DB: 14 Gaps: 59
Cy 620 GLYTYrTyrLeuGLYMet 625	1868 CCTGATGCTGAGCTCTCGGCTTTACAACCTGCTACCAGAAAAGGACCTCACT	1811 GCTCCTCAGTCCGTCTGCGCCCTCCGTGCTGCAAAGCCGTGCTCATGAAG	TOTAL TENNET POINT POI	TO SELLIFORE TRESPONDE TO THE CONTROL OF THE CONTRO	1631 GIGANGTEREVERSE TERMINE TERMINE TERMINE TERMINE TERMINE THE STREET THE S	511	493 LentysGluteuSerTyrmetValValSerArgGlyGlnLeuValAlaValGly	1451 TGTGGCCATACTCAGACAGTCCAGGCACATTATATTCTGAATGGAGGCACCCTGCTGGGG	459 1391 470	1367 GAAGAGGCACATCACATTAT	1307 AGGGTCAATTACAAGGATCGTAGTCCCTGTTACGGCTACCAGTGGGTGTCAGAAGAACAC	OV 429 IVSIleGluPhePro	ь	Db 1148 GTGCGCCTAGTAGATGGGAAAGGCGTCCCTATACCAAATAAAGTCATA 1195 Ov 392 ThrValThrGlnArgAsnTvrThrGluTvrTrpSerGlvSerAsnSerGlvAsnGlnLvs 411	Qy 372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle 391	Qy 352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371 1133 CCCTTCTTTGGGCAG 1147		1025 GAAGAAGGAACAGTGGTGGAATTGACTGGAAGGCAGTCCAGTGAAATCACAAGAACCATA	Db 989 TATGAAATGAAACTTCACACTGAGGCCCAGATCCAA 1024 Oy 317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331

LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln :::	ThrValThrAlaLeuSer	ATTCGTGAG GluValLysV CGGGTCAGTG CAAGCGCCTC CAAGCGCCTC	ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr	PheMetAgnSerPheAla :::: TATATTAATTGAAATCACATATACTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC ValPheGlnGluCygGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle ::::: TTCCTAGAGGACATGGGCTTAAAGGCATCACCAACTCAAAGTTCGTAAACCCAAATG AspGlyValTyrAspAsnAlaGluTyr TGTCCACAGCTTCAACAGTATGAAATGCATGAAAGTTCGTGAAGTTTTTAT AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu GAGTCAGATGTAATGGAAGAGCCATGCACGCCTGGAGACTTCGAAGAGTCTTCGAGAT AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu	
Qy 1216 SerProLeuAlaValValGln	Qy 1160 GluGlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175	Qy 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrp 1124	Qy 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsmIleAspValGlnGluSerIleHisPhe 1074 ::: Db 3365 GCCCTTCTGGAGATTCCTCTCACAGTCACTCTGTCGCAATGCCCTGTTTTGC 3424 Qy 1075 LeuGluSerGluPheSerArgGlyIleSerAspAsmTyrThr 1088	Db 3005 GATTATCTAAATGAAACACAGCAGCTTACTCCAGAGATCAAGGCCATTGGCTAT 3064 Qy 957 MetargGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976 Qy 957 MetargGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976	937 BenTu

72	Qy 52 CysProSerGlnValThrValLysAlaGluLeuLysThrAlaSerAsnLeuThrVal 71	Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51		-10-020-095-4 (1-1428) x US-09-873-403-4 (1-4422)	y Match: 19.60% Indels: 9 Gaps:	Pred. No.: 3.36e-133 Length: 4422 Score: 1440.00 Matches: 451 Percent Similarity: 46.20% Conservative: 266 Best Local Similarity: 29.06% Mismatches: 551	; ORGANISM: Homo sapiens US-09-873-403-4 Alignment Scores:	; SEQ ID NO 4 ; LENGTH: 4422 ; TYPE: DNA	; SOFTMAR C. FASTSEQ for Windows Version 3.0		; FILE REFERENCE: 8449-178 ; CURRENT APPLICATION NUMBER: US/09/873,403 ; CURRENT FILING DATE: 2001-06-04 ; PRIOR APPLICATION NUMBER: 09/625,139	; GENERAL INFORMATION: ; APPLICANT: STIVSTAVA, Pramod K ; TITLE OF INVENTION: COMPLEXES OF ALPHA (2) MACROGLOBULIN AND ANTIGENIC ; TITLE OF INVENTION: MOLECULES FOR IMMUNOTHERAPY	RESULT 5 US-09-873-403-4 ; Sequence 4, Application US/09873403 ; Patent No. US20020028207A1	Qy 1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380	QY 1349 ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368 :::::::::	Qy 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348 ::: :: 15	CY 1312 GINAIA11686rLeuSerGluThrValLysLysValGluTyrAspHisGly 1328	4163 TCTGCCTCCAACATGGCGATCGTT	4103 GAACCCAAAGCCCACACCAGCTTCCAAATCTCCCTAAGTGTCAGCACACAGGGAGCCGC	1276 AspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyProGly	Db 4043 CCAGAAAGGAAGATTCCCCTTTGCTTTAGGAGTGCAGACTCTGCCTCAAACTTGTGAT 4102
- 2γ	dd VQ	Db .	Q B	8	β Q	Db Qy	D Q	Db	γQ	Db Qy	B &	D Q	D Q	B &	සි රි	אס ממ	Db .	B 75	Вb	δ	Db
392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411	372 ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle 391	 90 CCCTTCTTTGGGCAG	1042 ACCAAACTCTCATTTGTGAAAGTGGACTCACACTTTCGACAGGGAATT 1089 352 GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371	32 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316	277 LysLysAsnileThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296	850 CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA 909	272SerpheTrpGlyLys 276	264 ValThrLeuThrPheLeuProLeu	244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::: ::: ::::::	224 TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 :::	206 IleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223 :::	186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205	167 LeuIleLyBASpProLySSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185 	147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166	127 LysargIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 146 	10/ Intertyrighter happetulle leutreser Asser interqueuser rheef ivin 126		90 LeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgVal 106	:::

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IleTrpLeu arcrgggar	661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	652 AspGlyValTyrAspAsnAlaGlu	632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651 ::::::	626 PheMetAsnSer	GlyTyrTyrLeuGlyMet	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr 619 ::::::::::::::::::::::::::::::::: ::::: 1825 CCTGATGCTGAGCTCTCGGGGTCCTCGGTTTACAACCTGCTACCAGAAAAGGACCTCACT 1884	581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600	561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580	541 GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys 560 ::::::	521 ProGluAsnSerTrpThrProLysAlaCysVallleValTyrTyrIleGluAspAspGly 540 :::::	511	493 LeuLy8GluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510	479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492	459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478	439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458	429 LysileGluPheProIleLeuGluAspSer 438 ::::::	412 MeCGLUALAVAIGITLYSILEASHTYTTHTVALPTOGINSETGLYTHPHe 428	TTCATCAGAGGAAATGAAGCAAACTATTACTCCAATGCTACCACGGATGAG
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1015 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgVallle 1034		3082 TITGGGAAGGATATGGCAGGAACCAGGGCAACACCTGGCTCACAGCCTTTGTTCTGAAG 3141	WetArgGinGlyTyrGinArgGiuLeuLeuTyrGinArgGiuAgggiySerPneSerala		MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu	897 IleThrAlaileGlyAspValLeuGlyProSerIleAsnGLyLeuAlaSerLeuIleArg 916 :::::: ::: ::: 2842 GTCTCAGTTTTGGGAGACATATTAGGCTCTGCCATGCAAAACCACAAAATCTTCTCCAG 2901	Leurystrictensetphesetphespopposastication to the control that the control	CluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr	CCTGAACACGGAAGGAAAGACACAGTCATCAAGCCTCTGTTGGTTG	Intralling Albert	GLUASPGLYALATINIVALLEUPNEVETLEARGPFOTNIKHSLEUGLYGLULLEPTOLLEACTGTGTCCTGGGCAGTAACCCCAAAGTCATTAGGAAATGTGAATTTC	GAACAAGCGCCTCACTGCATCTGTGCAAACGGCGGCAAGAACAAGCGCCTCACTGCATCTGTGCAAACGGCGGCGAA	ThrGITVALLYSVALITETIEGIULYSSERASDIJSPARASDITELEUMGETTNISERSER					698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717

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1176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3559 CAGAAACCCAAGGCACCAGTGGGGCATTTTTACGAACCCCAGGCTCCCTCTGCTGAGGTG
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                                                   4240 CATGTCTTGATTTÄCCTTGÄTAAGGTGTCAAATCAGACACTGAGCTTGTTCTTCACGGTT
                                                                                                                                                                                                                 1312 GluAlaIleSerLeu------SerGluThrValLysLysValGluTyrAspHisGly 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1216 SerProLeuAlaValGln------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys-----GluAsnLysAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIle 1258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGCCACATTTACC---AGGACTGGGAAGGCTGCACAGGTGACTATCCAGTCTTCAGGG 3852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla 1195
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ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTyr 1368
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                                                                                                          LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla
                                                                                                                                                                                                                                                                                                                               ---ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer
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                                                                                                                                                                 CCAACAGTGAAAATGCTTGAAAGATCTAACCATGTGAGCCGGACAGAAGTCAGCAGCAAC
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US-09-873-403-3
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CURRENT APPLICATION NUMBER: US/09/873,403
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/625,139
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: 60/209,266
PRIOR FILING DATE: 2000-06-02
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 4577
TYPE: DNA
TYPE: DNA
TO ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: STIVESUAR, Pramod K
TITLE OF INVENTION: COMPLEXES OF ALPHA (2) MACROGLOBULIN
TITLE OF INVENTION: MOLECULES FOR IMMUNOTHERAPY
FILE REFERENCE: 8449-178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09873403 Patent No. US20020028207A1
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                                                                                                                                                          167 Leu---IleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp
                                                    476 AAATTTCGTGTTGTCTCCATGGATGAAAACTTTCACCCCCTGAATGAGTTGATTCCACTA
                                                                                                     147 LysPheArqIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle
                                                                                                                                                                                                                                                                     365 AAAGGACCAACCCAAGAA------TTTAAGAAGCGGACCACAGTGATGGTTAAGAAC
                                                                                                                                                                                                                                                                                                                                                                        311 -----GCTGTCCCAAAGTCTTCATCCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                       90 LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis
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                                                                                                                                                                                                                                                                                                                    ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr
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479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492	LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys		LysIleGluPhePro	MetGluAlaValGlnLysileAsnTyrThrValProGlnSerGlyThrPhe	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys	SpGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 		ValThrLeuThrPheLeuProLeu	244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysDroValLysGlyAsp 263 ::: ::: ::::::	224 TyrValleuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 :::	206 IleGlnValAgnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223 ::: :::	186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205	::: :::
Db 2507 AT	758 Va 2447 GT	Qy 738 Th	Qy 718 Th	Qy 698 As	Qy 681 Gl Db 2219	Qy 661 Al Db 2168 GA	Qy 652 As	Qy 632 Va Db 2048 TT	Qy 626 Ph :: Db 1988 TA	620 1928	Oy 601 A1	Oy 581 Th Db 1811 GC	Qy 561 Le Db 1751 TT	Qy 541 G1 :: Db 1691 GA	521 1631	1571	1511	. 1451
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1075 LeuGluSer	1035 HisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054 ::::::::::::::::::::::::::::::::::::	995 CysPheLeuGluAlaAspProTyrIleAspGlnAspGlnAsnValLeuHisArgThrTyr 1014	957 MetargGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976 :::	917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936	877 LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln 896 :::	842SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856 2714 CCTGAACACGGAAGGAAAGACACAGTCATCAAGCCTCTGTTGGACCTGAAGCACTA 2773 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876	798 Glu
US-09-880-107-2236 ; Sequence 2236, Application US/09880107 ; Patent No. US20020142981A1 ; GENERAL INFORMATION: APPLICANT: Horne, Darci T. APPLICANT: Vockley, Joseph G. APPLICANT: Scherf, Uwe ; APPLICANT: Gene Logic, Inc. TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO ; CURRENT APPLICATION NUMBER: US/09/880,107 ; CURRENT FILING DATE: 2001-06-14	Oy 1349 VALAEGASHPHELYSVALSERASHALASETVALSELLEVALASHYTTY 1368 :::::::	1312 GIMAGATRE CENTRAL PERSONAL TRAILING WALLES WALLED TO THE PROPERTY OF THE	1276 ABPLEUABRTH.SVALABPLEUABRIVALCYSTHYSERPHESERGLYPTOGLY	1239 GINLE 1016 CAGAC 1259 GINAB 4043 CCAGAC	1216 SerProLeuAlaValValGIn	Db 3779 GGCGCCACATTTACCAGGACTGGGAAGGCTGCACAGGTGACTATCCAGGTCTTCAGGG 3895	1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIle ::::::::::::::::::::::::::::::::::::

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PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2236
LENGTH: 4577
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 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263
                                                                                                                                                                                                   LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205
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                                                                                                                              IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu
                                  TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA
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                                                                                 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly
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833 ThrValThrAlaLeuSer	798 Glu	758 ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla	718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr	681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu	652 AspGlyValTyrAspAsnAlaGluTyr	626 PheMetAsnSerPheAla ::::: 1988 TATATTAATGAATCACATATACTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC 632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle :::::	601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr ::::::::::::::::::::::::::::::::::::	1691 GACGTGATTGGGGATTCTGCAAAATATGATGTTGAAAATTGTCTGGCCAACAAGGTGGAT 1750 561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580
941 Oy 2713 Db 2773 Oy Db	812 Qy 2605 Db 832 Qy 2653 Db	777 Qy 2506 Db 797 Qy 796 Db	737 Db 2389 Qy 757 Db 2446 Db	697 Db 2269 Qy 717 Db	660 Oy 2167 Ob 680 Op 2218	631 Qy 2047 Db 2017 Qy 651 Db	619 Db 1927 Qy 625 Db	? B Q B Q
1160 GlucilyilePro	ValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIle ::::::::::::::::::::::::::::::::::::	1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla 1107	105 SETLEULEUGLYTYRARGLYBTYRGINPROASNILEASDVALGINGLUSETILEHISPHE 1074 ::: 3365 GCCCTTCTGGAGATTCCTCTCACAGTCACTCACCCTGTTTGTCCGCAATGCCCTGTTTTGC 3424 1075 LeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr 1088	INTITUDENTY SELIMITY SERVANDES OF THE PROPERTY	PheGlyAsnTyrAspProSerGlySerThrTxpLeuSerAlaPheValLeuArg		2945 ATGCCCTARGCTGTGGAGAGCAGAATATGGTCCTCTTTGCTCCTAACATCTTATGTACTG 3004	GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr

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APPLICANT: HILLAN, KENNETH J
APPLICANT: PHILLIPS, HEIDI S
APPLICANT: POLAKIS, PAUL
APPLICANT: SMITH, VICTORIA
APPLICANT: SPENCER, SUSAN D.
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                                                                                          CURRENT APPLICATION NUMBER: US/10/331,496A CURRENT FILING DATE: 2002-12-30 PRIOR APPLICATION NUMBER: US 60/345,444 PRIOR FILING DATE: 2002-01-02 PRIOR APPLICATION NUMBER: US 60/351,885 PRIOR APPLICATION NUMBER: US 60/360,066 PRIOR APPLICATION NUMBER: US 60/360,066
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                  PRIOR
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              OR APPLICATION NUMBER: US 60/345,444
OR FILING DATE: 2002-01-02
OR APPLICATION NUMBER: US 60/351,885
OR FILING DATE: 2002-01-25
OR APPLICATION NUMBER: US 60/360,066
OR FILING DATE: 2002-02-25
OR APPLICATION NUMBER: US 60/362,004
OR FILING DATE: 2002-03-05
OR APPLICATION NUMBER: US 60/366,869
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SPENCER, SUSAN D.
WILLIAMS, P. MICKEY
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PRIOR FILING DATE: 2002-03-21
PRIOR APPLICATION NUMBER: US 60/368,679
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/404,809
PRIOR FILING DATE: 2002-08-19
PRIOR FILING DATE: 2002-08-21
PRIOR FILING DATE: 2002-08-21
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NUMBER OF SEQ ID NOS: 95
SEQ ID NO 19
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                  TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA
                                                                                              GTGGTGGTACAGAAGAAATCAGGTGGAAGGACAGAGCAC
                                                                                                                                   IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu
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833 ThrValThrAlaLeuSer	
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778 ThrGluVallysValIleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer	479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492
758 ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 	459 LeuPheLysSerProSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478
	AGGGTCAATTACAAGGATCGTAGTCCCTGTTACGGCTACCAGTGGGTGTCAGAAGAACAC 1366 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458
2270 TIGGTGGTGGTAACTCAGCAGGGGTGGCTGAGGTAAGAGTCACGTCCTGACACCATC 718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr	CATGGCCTTGTACAGTTCTCTATCAACACCACCAACGTTATGGGTACCTCTCTT Ly81leGluPhePro
681 GLySerSerProH18	erGlySerAsnSerGlyAsnGlnLys
	spGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle 391
652 ABPG1yValTyrAspAsnAlaGluTyr	laThrValLys ::: CAG
632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle ::::::	ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle
626 PheMetAsnSer	
620 GlyTyrTyrLeuglyMet	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316
601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr ::::::::::::::::::::::::::::::::::::	
581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600	
561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580	
:::::: ::: 1691 GACGTGATTGGGGATTCTGCAAAATATGATGTTGAAAATTGTCTGGCCAACAAGGTGGAT 1750	244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::: ::: ::::::

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                                                                                                                                            GAGGACCTGACCTCTGCAACCAACATCGTGAAGTGGATCACGAAGCAGCAGAATGCCCCAG
                                                                                                                                                                                                                                                                                                                                                            GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGln-----ThrSer 1159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySer---ProLysAlaLysGluAla 1107
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APPLICANT: Waga, Iwao
APPLICANT: Wamamoto, Jun
APPLICANT: Yamamoto, Jun
TITLE OF INVENTION: Identifying Drugs for and
TITLE OF INVENTION: Hyperplasia Using Gene Ex
FILE REFERENCE: 44921-5029-US
FULRENT APPLICATION NUMBER: US/09/873,319A
CURRENT APPLICATION NUMBER: US 60/223,323
EARLIER APPLICATION NUMBER: US 60/223,323
EARLIER FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 755
COCTUBER: US 60 JENSEL PORTION OF SEQ ID NOS: 755
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      US-09-873-319-408
                                                                                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 408
LENGTH: 4577
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Publication No. US200
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 408, Application US/09873319A Publication No. US20030134324A1
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Munger, William E. APPLICANT: Kulkarni, Prakash APPLICANT: Getzenberg, Robert
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Genbank Accession No. US20030134324A1 M11313
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Db 953 GTAÀAAACCAAGGTCTTCCAGCTGAAGAGGGAAGGAG 988	Qy 277 LysLysAsnIleThrLysThrPheLysIleAsnGlySérAlaAsnPheSerPheAsnAsp 296	893 CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA	272SerPheTrpGlVLvs	QY 264 ValThrLeuThrPheLeuProLeu	Qy 244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::: ::: :::::	713 TTTGTTCCTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA	OV 224 TyrValieuproiysphediuvalThrieudlnThrproieumTyrCysgerMetAsnser 243	206 IleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu	Qy 186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205	536 GTATACATTCAGGATCCCAAAGGAAATCGCATCGCACAATGGCAGAGTTTCCAGTTAGA	ProLysSerAsnLeulleGlnGlnTrpLeuSerGlnGlnSerAsp 18	QY 147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166		127 LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal 14	Qy 107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126	311GCTGTCCCAAAGTCTTCATCCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG 3	90 LeuProSer	72SerValLeuGluAlaGluGlyValPheGluLy8GlySerPheLy8ThrLeuThr 89 :::	Db 203 CTGAATGAGACAGTGACTGTAAGTGCTTCCTTGGAGTCTGTCAGGGGAAACAGGAGCCTC 262	146 GTCCCCTCCCTGCTCCACACTGAGACCACTGAGAAGGGCTGTGTCCTTCTGAGCTAC	Qy 32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51	Qy 12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31 ::: ::::	US-10-020-095-4 (1-1428) x US-09-873-319-408 (1-4577)	y Match: 19.60% Indels: 13 Gaps:	Pred. No.: 3.56e-133 Length: 4577 Score: 1440.00 Matches: 451 Percent Similarity: 46.20% Conservative: 266 Best Local Similarity: 29.06% Mismatches. 551
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917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936 ·	897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916 :::::: ::: :::::::::::::::::::::	877 LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln 896 :::	GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr :::	SeraspalavalThrGlnMetIleLeuValLysalaGluGlyIle 	ThrValThrAlaLeuSer	GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle	GALCAAGCGCCTCACTGCATCTTGCAAACGGGGGGCAAGAACAAGCGCCTCACTGCATCTTGCAAACGGGGGGCAA	ThrGluValLysValllelleGluLysSerAspLysPheAspIleLeuMetThrSerSer	ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 	738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757	718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 737	698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717 :::	681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu 697	661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	652 AspGlyValTyrAspAsnAlaGlu	632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651	626 PheMetAsnSer	::: 1928 GGCTTCCCTGGGCCTTTGAATGACCAGGACGATGAAGACTGCATCAATCGTCATAATGTC 1987
Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIle 1258	TTGCCAGAGCTGCCTGGGGAATACAGCATGAAAGTGACAGGAAGGA	1216 SEPPROLEUALAVALVALGIN	1196 AlaLeumetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro	Qy 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLy8AlaLeuSerGluPheAla 1195	Qy 1160 GluGlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeu 1175	Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSer 1159	Qy 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIle 1142	Qy 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrp 1124	Qy 1089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla 1107	Qy 1075 LeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr 1088	1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe ::: :::::::::::::::::::::::::	Qy 1035 HisSerGluLeuGlnGlyGlyAsnLy8SerProValThrLeuThrAlaTyrIleValThr 1054		CyBERGLEUGIUNIAMBPETCHYTILEMSPILEMSDGITASHVALLEUNISMIGITTYT ACTITIGCCCAAGCCTCGAGCCTACATCTTCATCGATGAAGCACACACA	9// PREGIYABITYKASPPIOSEIGIYSEINTIPLEUSEIKAAPREVAILEUKIG 	3065 CTCAACACTGGTTACCAGAGACAGTTGAACTACAAACACTATGATGGCTCCTACAGCACC	3005 GATTATCTAAATGAAACAGCAGCTTACTCCAGAGGTCAAAGTCCAAGGCCATTGGCTAT	2945

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PRIOR APPLICATION NUMBER: 60/223,323
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 09/873,319
PRIOR FILING DATE: 2001-68-05
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 654
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TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplas
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5029-01US
CURRENT APPLICATION NUMBER: US/09/960,706
CURRENT FILING DATE: 2001-09-24
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   CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal
                                         GTCCCCTCCCTGCTCCACACT---GAGACCACTGAGAAGGGCTGTGTCCTTCTGAGCTAC
                                                                            AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51
                                                                                                                  CTCTTGGTCCTCCTGCCCACAGACGCCTCAGTCTCTGGAAAACCGCAGTATATGGTTCTG
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ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle
                                                                                                                                                                                                                                                                                                                       GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ValThrLeuThrPheLeuProLeu------
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                                                                                                                                                                                                           GAAGAAGGAACAGTGGTGGAATTGACTGGAAGGCAGTCCAGTGAAATCACAAGAACCATA
                                                                                                                                                                                                                                                                                          TATGAAATGAAA-
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                                                                                            GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys 371
                                                                                                                                  ACCAAACTCTCA---TTTGTGAAAGTGGACTCACACTTTCGACAGGGA-----ATT
                                                                                                                                                                   ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351
                                                                                                                                                                                                                                              SerProGlyProValGluIleLeuThr------ThrValThrGluSerVal 331
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Qy 957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976 ::: :::	Qy 897 ITETITALALIECTYABPVALLEUGTYFTOSEFILEABHUTYLEUALTSETLEULTEARY 916 2885 GTCTCAGTTTTGGGAGACATATTAGGCTCTGCCATGCAAAACACACAAAATCTTCTCCAG 2944 Qy 917 MetProTyrGlyCysGlyGluGlnAsmMetIleAsnPheAlaProAssnlleTyrIleLeu 936	857 GluLy 2774 GAGAA 877 LeuLy :: 2828GA	Qy 833 ThrValThrAlaLeuSer	Qy 798 Glu	Qy 758 ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777	Qy 681 GlySerSerProHis

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                                                                                                                                                                                                              TCTGCCTCCAACATGGCGATCGTTGATGTGAAGATGGTCTCTGGCTTCATTCCCCTGAAG
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LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348
                                                                    CCAACAGTGAAAATGCTTGAAAGATCTAACCATGTGAGCCGGACAGAAGTCAGCAGCAAC
                                                                                                                                      GluAlaIleSerLeu------SerGluThrValLysLysValGluTyrAspHisGly 1328
                                                                                                                                                                                                                                                                               ---ArgSerGlyMetAlaLeuMétGluValAsnLeuLeuSerGlyPheMetValProSer 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCAGAAAAGGAAGAGTTCCCCCTTTGCTTTAGGAGTGCAGACTCTGCCTCAAACTTGTGAT 4102
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US-10-292-081A-3
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DB:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3
LENGTH: 4577
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APPLICANT: Aleister J. Saunders
TITLE OF INVENTION: SINCLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGIA
FILE REFERENCE: 37481-3323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Kenneth David Becker
APPLICANT: Gonul Velicelebi
APPLICANT: Xin Wang
APPLICANT: Randolph B. Tanzi
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1369 GluProArgArgGlnAlaValArgSerTyrAsnSer 1380
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  416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 AlaproGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51
LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal
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GAGGACAGTCTGGTCTTTGTCCAGACAGACAAATCAATCTACAAACCAGGGCAGACAGTG
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                                                                                    AAAGGACCAACCCAAGAA----
                                                                                                                                                             TTCACTGACCTGGAGGCGGAGAATGACGTACTCCACTGTGTCGCCTTC
                                                                                                                                                                                                                                                                                        ---SerValLeuGluAlaGluGly---ValPheGluLysGlySerPheLysThrLeuThr 89
                                                                                                                                                                                                                                                                                                                                                                       CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal 71
                                                                                                                                                                                                                                                                                                                                                                                                                  GTCCCCTCCCTGCTCCACACT---GAGACCACTGAGAAGGGCTGTGTCCTTCTGAGCTAC
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                                                                                                                    ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126
                                                                                                                                                                                                        LeuProSerLeuProLeuAsnSerAlaAspGlu-----IleTyrGluLeuArgVal 106
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SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer GAAGAGGCACATCACACTGCTTAT	412 MetGluAlaValGlnLy8IleAsnTyrThrValProGlnSerGlyThrPhe 428	1148 GTGCGCCTAGTAGATGGGAAAGGCGTCCCTATACCAAATAAAGTCATA 1195 392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411 392 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411 1196 TTCATCAGAGGAAATGAAGCAAACTATTACTCCAATGCTACCACGGATGAG 1246	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	953 GTAAAAACCAAGGTCTTCCAGCTGAAGAGGAAGGAG 988 297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316 989 TATGAAATGAAA	LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp	244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::: :: :::	656 GTGGTGGTACAGAAAATCAGGTGGAAGGACAGAGCCCTTTCACCGTGGAGGAA 712 224 TyrValLeuProLygPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer 243 ::: 713 TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA 772	186 LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205 186 LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205 596 GGTGGCCTCAAGCAATTTTCTTTTCCCCTCTCATCAAGCCCTTCCAGGGCTCCTACAAG 655 206 IleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223 :::	LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle ::: ::::: AAATTTCGTGTTGTCTCCATGATGAAAACTTTCACCCCCTGAATGAGTTGATTCCACTA
Qy 738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757	ThrsetTrpValAlaThrGlyPheValIleserGluAspLeuGlyLeuThrThrThrThrThrThrThrThrThrThrThrThrThrT	681 2219	Qy 652 AspGlyValTyrAspAsnAlaGluTyr 660 Db 2108 TGTCCACAGCTTCAACAGTATGAATGCATGGAACGTCTAACGTGTAGGTTTTTAT 2167 Qy 661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	1988 632 2048	Qy 620 GlyTyr	Db 1811 GCTCCTCAGTCCGTCTGCGCCTCCGGTTTACAAGCGTGCTGCTAGAAGGACCTACAT Qy 601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr 619 :::::::::::::::::::::::::::::::::::	1691 GACG	521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly	Qy 493 LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510	Qy 459 LeuPheLysSerFyoSerLysThrTyrIleGlnLeuLysThrArgAspGluAsnIleLys 478

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	1035 HisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054 ::::::: 3305 AACAATGCCATAAAGGAAGATGAAAATGAAGTGACCCTCTCCGCCTATATCACCATC 3364 1055 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe 1074 ::: ::: 3365 GCCCTTCTGGAGATTCCTCTCACAGTCACTCACCCTGTTGTCCGCAATGCCCTGTTTTGC 3424	15 ThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPheTrpAspProGlyArgValIle	7 - F	957 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla 976 :::	937 AspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGluLysAlaLeuSerPhe 956 ::: :: ::: ::: 3005 GATTATCTAAATGAAACACAGCAGCTTACTCCAGAGGTCAAGTCCAAGGCCATTGGCTAT 3064	917 MetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu 936 	897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg 916 :::::: ::: :::::: 2885 GTCTCAGTTTTGGGAGACATATTAGGCTCTGCCATGCAAAACACACAAAATCTTCTCCAG 2944	877 LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln 896 :::	857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876	SeraspalaValThrGlnMetIleLeuValLysalaGluGlyIle		813 GluaspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832	798 Glu	778 ThrGluValLysVallleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797	
RESULT 12 US-10-292-081A-5 (VS-10-292-081A-5) ; Sequence 5, Application US/10292081A ; Publication No. US20030162202A1 ; GENERAL INFORMATION: ; APPLICANT: Kenneth David Becker ; APPLICANT: Gonul Velicelebi	4343 CTGCAAGATGCCAGTAAGAGATCTCAAACCAGCCATAGTGAAAGTCTATGATTACTAC 1369 GluproArgArgGlnAlaValArgSerTyrAsnSer 1380	Qy 1329 LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla 1348 ::: :: Db 4283 CATGTCTTGATTTACCTTGATAAGGTGTCAAATCAGACACTGAGCTTGTTCTTCACGGTT 4342 Ov 1349 ValArgAsnPheLysValSerAsnThrGlnAsnAlaSerValSerTleValAsnTvTvr 1368	Db 4163 TCTGCCTCCAACÁŤĠĠĠATCGTTGATĠŤĠAAGATGGTCŤĠĠĊŤŤĊATTCCCCTGAAG 4222 Qy 1312 GluAlaIleSerLeuSerGluThrValLysLysValGluTyrAspHisGly 1328	Db 4103 GAACCCAAAGCCCACACCACCACCTCCAAATCTCCCTAAGTGTCAGTTACACAGGGAGCCGC 4162 Qy 1293ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer 1311	1259 GlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLysAsp	Qy 1239 GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgSerIle 1258	Qy 1223ProMetAlaValAsmIleSerAlaAsmGlyPheGlyPheAlaIleCys 1238	Qy 1216 SerProLeuAlaValValGln 1222 ::: Db 3896 ACATTTTCCAGCAAATTCCAAGTGGACAACAATCGCCTGTTACTGCAGCAGGTCTCA 3955	Qy 1196 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro 1215	Qy 1176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLy8AlaLeuSerGluPheAla 1195	Qy 1160 GluGlyIlePro	Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSer 1159	Qy 1125 ValSerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIle 1142	Oy 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrp 1124	3482

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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 5
LENGTH: 4577
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT:
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APPLICANT: Aleister J. Saunders
TITLS OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGL
FILE REFERENCE: 37481-3323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/337434
PRIOR APPLICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
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TyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSerMetAsnSer
                                 GTGGTGGTACAGAAGAAATCAGGTGGAAGGACAGAGCAC---CCTTTCACCGTGGAGGAA
                                                                 IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu
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521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly :::::: | | | | ::: | | | | :::
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                                                                                                                                                                                                                                                                                                                            GAAGAGGCACATCACACTGCTTAT---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys 411
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                                                                                                                                                      LeuLysGluLeuSer-----TyrMetValValSerArgGlyGlnLeuValAlaValGly
                                                                                                                                                                                                                       ValGlySer-----ProPheGluLeuValValSerGlyAsnLys-----Arg
                                                                                                                                                                                                                                                          CTTGTGTTCTCCCCAAGCAAGAGCTTTGTCCACCTTGAGCCCATGTCTCATGAACTACCC 1450
                                                                                                                                                                                                                                                                                                                                                          SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer
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                                                                                                                      CTGAAGAAGCTCTCCTTTTATTATCTGATAATGGCAAAGGGAAGGCATTGTCCGAACTGGG
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                                                                                      -MetPheSerLeuThr 520
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798 Glu	758 ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777 [ASPTHYASIMETGLYTYPATGLIFF TO THE TRANSPORT OF THE TRANSPO	TICCTAGAGGACATGGGCTTAAAGGCCATTCACCAACTCAAAGATTCGTAAACCCAAATG AspGlyValTyrAspAsnAlaGluTyr TGTCCACAGCTTCAACAGTATGAAATGCTTTTTAT AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu	1868 CCTGATGCTGAGCTCTCGGCGTCCTCGGTTTACAACCTGCTACCAGAAAAGGACCTCACT 1927 620 GlyTyr	GIUIIeIleSerAspvalLeuLysIleProValGlnLeuValPheLysAsnLysIleLys
Qy 1125 ValserSerGliSerLysLeuSerAspSerTrpGlnProArgSerLeuAspI1e 1142 Db 3602 CAGAAACCCAAGGCACCAGTGGGGCATTTTTACGAACCCCAGGCTCCTCTGCTGAGGTG 3661 Qy 1143 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSer 1159	3425 CTGGAGTCAGCCTGGAAGACAGCACAAGAAGGGGACCATGGCAGCCATGTATATACC 1089 LeuAlaLeu1leThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla ::: 3482 AAAGCACTGTGTGTGTTTTTCCCCTGGCAGGACAAGACAAGAGAAGAAGAAGAAGATA 1108 LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrp 3542 CTCAAGTCACTTAATGAGGAAGCTGTGAAGAAGACAACTCTGTCCATTGGGAGCGCCCT	Db 3245 ATATGCTCTCCCAGAGGCAGAGGACAATGCTGTTTCAGGAGCTCTGGGTCACTGCTC 3304 Oy 1035 HisserGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrIleValThr 1054 :::::::::::::::::::::::::::::::::::	Db 3065 CTCAACACTGGTTACCAGAGACAAGTTGAACTACAACTATGATGGCTCCTACAGCACC 3124 Qy 977 PheGlyAsnTyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArg 994		Qy 842SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856 2714 CCTGAACACGGAAAGACACAGTCATCCAAGCCTCTGTTGGATGAACCTGAAGGACTA 2773 Qy 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876

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FILE REFERENCE: 50665-8021.US00
CURRENT APPLICATION NUMBER: US/10/076,816
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,188
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR PRICATION NUMBER: US 09/847,232
PRIOR PRILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: US 60/266,929
PRIOR APPLICATION NUMBER: US 60/201,182
PRIOR APPLICATION NUMBER: US 60/201,182
PRIOR PRIOR DATE: 2000-05-02
INUMBER OF SEQ ID NOS: 60
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 56
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/10076816 Publication No. US20030056244A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               APPLICANT: Huang, Ning
APPLICANT: Rodiguez, Raymond
APPLICANT: Hagis, Frank E.
TITLE OF INVENTION: Feed Additive Compositions
LENGTH: 4577
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 AlaproGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr
                                                                                                                                      ValThrLeuThrPheLeuProLeu---
                                                                                                                                                                                                   LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp
::: :::||| :::::
                                                                                                                                                                                                                                                                                IleGlnValGlnValAsnAsp-----GlnThrTyrTyrGlnSerPheGlnValSerGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuGlyValIleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leu---IleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysArgIleSerValPheIleGlnThrAspLysAlaLeuTyrLysProLysGlnGluVal
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                      CAGGCTTTCTGTGAGAAATTCAGTGGACAGCTAAACAGCCATGGCTGCTTCTATCAGCAA
                                                                                                                                                                            GAAGAGATGAATGTATCAGTGTGGGCCTATACACATATGGGAAGCCTGTCCCTGGACAT
                                                                                                                                                                                                                                                            TTTGTTCTTCCCAAGTTTGAAGTACAAGTAACAGTGCCAAAGATAATCACCATCTTGGAA
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                                                                                                   GTGACTGTGAGCATTTGCAGAAAGTATAGTGACGCTTCCGACTGCCACGGTGAAGATTCA
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1811 GCTCCTCAGTCCGTCTGCGCCCCTCCGTGCTGGACCAAAGCGTGCTGCTCATGAAG 1867 601 AlaSerAsnAspIleThrMetGluAsnValWisGluLeuGluLeuTyrAsnThr 619	ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn	LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 	GluIleIleSerAspValLeuLysIleProValGlnLeuValPheLysAsnLysIleLys :::::	ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly		LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly	ValGlySerProPheGluLeuValValSerGlyAsnLysArg	LeuPheLysSerProSerLysThrTyrlleGlnLeuLysThrArgAspGluAsnIleLys	SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer		MetGluAlaValGlnLyslleAsnTyrThrValProGlnSerGlyThrPhe	ThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLys ::::	ValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValVallle	GluPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys CCCTTCTTTGGG	332 ThrGlyIleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIle 351 :::	317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	297 GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer 316	277 LysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAsp 296
897 IleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerLeuIleArg	Qy 877 LeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluArgValGln 896	Qy 857 GluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGlnSerThr 876 :::::: :::::::::::::::	Qy 842SerAspAlaValThrGlnMetIleLeuValLysAlaGluGlyIle 856	Qy 833 ThrValThrAlaLeuSer	Qy 813 GluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGluIleProIle 832	Qy 798 GluIleAsnAlaThrGlyHisGlnGlnThrLeuLeuValProSer 812	Qy 778 ThrGluValLysVallleIleGluLysSerAspLysPheAspIleLeuMetThrSerSer 797	Qy 758 ValileArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAla 777	Qy 738 ThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSer 757	Qy 718 ThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGlyLeuThrThr 737	Qy 698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717	Qy 681 GlySerSerProHisValArgLysHisPheProGluThrTrpIleTrpLeu 697	Qy 661 AlaGluArgPheMetGluGluAsnGluGlyHisIleValAspIleHisAspPheSerLeu 680	Qy 652 AspGlyValTyrAspAsnAlaGluTyr 660	Qy 632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651	Qy 626 PheMetashSerPheAla 631 :::::: 1988 TATATTAATGGAATCACATATACTCCAGTATCAAGTACAAATGAAAAGGATATGTACAGC 2047	1928 GCTTCCCTGGGCCTTTGAATGACCAGGACGATGAAGACTGCATCAATCGTCATAATGTC	1868 CCTGATGCTGAGCTCTCGGCTCTCGGTTTACAACCTGCTACCAGAAAAGGACCTCACT

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1222	SerProLeuAlaValValGln
1215 3895	6 AlaLeuMetAsnThrGluArgThrAsnIleGlnValThrValThrGlyProSerSerPro
	176 GlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAla
1175 3778	60 GluGlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeu
	3 GluValAlaAlaTyrAlaLeuLeuSerHisPheLeuGlnPheGlnThrSer ::: :: ::: ::
1142 3661	SerSerGluSerLysLeuSerAspSerTrpGlnProArgSerLeuAspIle
1124 3601	108 LeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrp
1107 35 41	089 LeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAla
	S LeuGluSerGluPheSerArgGlyIleSerAspAsnTyrThr
1074 3424	5 SerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAspValGlnGluSerIleHisPhe ::: ::: GCCCTTCTGGAGATTCCTCTCACAGTCACTCACCCTGTTGTCCGCAATGCCCTGTTTTGC
1054 3364	5 HisSerGluLeuGlnGlyĠlyAsnLysSerProValThrLeuThrAlaTyrIleValThr :::::::::::::::: 5 AACAATGCCATAAAGGGAGGAGTAGAAGATGAAGTGACCCTCTCCGCCTATATCACCATC
1034 3304	15 ThrTxpLeuLysGlyHisGlnLysSerAsnGlyGluPheTxpAspProGlyAxgValIle
1014 3244	CysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisArgThrTyr
994 3184	SerAlaPheValLeuArg ::: ACAGCCTTTGTTCTGAAG
976 3124	7 MetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerPheSerAla :::
	7 ASPTYrLeuThrLySLySGlnLeuThrAspAsnLeuLySGluLySAlaLeuSerPhe ::: ::: 5 GATTATCTAAATGAAACACAGCAGCTTACTCCAGAGGTCAAGTCCAAGGCCATTGGCTAT
936 3004	/GluGlnAsnMetIleAsnPheAlaProAsnIleTyrIleLeu ::: AGAGCAGAATATGGTCCTCTTTGCTCCTAACATCTACTACTG
2944	TTGGGAGACATATTAGGCTCTGCCATGCAAAACACACAAAAATCTTCTCCAG

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4 (1-142	Scores: .milarity: . Similarity: ;h:	19-965-178 2-965-178 2-178, Application Use 178, Application SANT: INCYTE GENOMICS SANT: SHIFFMAN, Richard SEILHAMER, Jef ANT: PORTER, Gordon ANT: MIKITA, Thomas TAI, Julie OF INVENTION: GENES EXFERENCE: PA-0025 PC TY APPLICATION NUMBER: TILING DATE: 20025 PC TY APPLICATION NUMBER: FILING DATE: 2000-04 COP SEQ ID NOS: 276 APPLICATION NUMBER: FILING DATE: 2000-04 COP SEQ ID NOS: 276 APPLICATION SEQ ID NOS: 276 APPLICATION: INCYTE SEG INFORMATION: INCYTE SEG INCOME.	GluProAr GAGACGGA	ValArgAs ::::::: CTGCAAGA	LysLeuAs ::: CATGTCTT	GluAlaIl :: CCAACAGT	Argse	AspLeuAsn- ::: GAACCCAAAG	GlnAsnGl :: CCAGAAAA	GlnLeuAs :: CAGACCTC
8) x US-10-240	3.87e-133 1440.00 46.20% 29.06% 19.60%	US/10240 924A1 S, INC. nd. nJ. EXPRESS TT US/10 2-10-04 4-05	GluProArgArgGlnAlaValArgSerTyrAsnSer 	nPheLysValSerA ; ; :TGTCCCAGTAAGAG	nLeuTyrLeuAspS ::: GATTTACCTTGATA	GluAlaIleSerLeu ;;; CCAACAGTGAAAATGCTTGAAA	rGlyMetAlaLeum :::: CAACATGGCGATCG	nHisValAspL AGCCCACACCAGCT	nGluAlaPheAspL ; ;GGAAGAGTTCCCCT	GlnLeuAsnValValTyrAsnValL
-965-178 (1-4809	Length: Matches: Conservative: Mismatches: Indels: Gaps:	65 D IN FOAM CELL 240,965 06		snThrGlnAspAlaSe ;; ;; ATCTCAAACCAGCCAT	erValAsnGluThrGl ::: AGGTGTCAAATCAGAC	SerGluThrValLy BATCTAACCATGTGAG	etGluValAsnLeuLe ::::: rrgargrgaagarggr	euAsnValCysThrSe ;;: CCAAATCTCCCTAAG	GlnAsnGlnGluAlaPheAspLeuAspValAlaValLys :::	alLysAlaSerGlySe :: [T
S	4809 451 266 551 581 59	DIFFERENTIATION	1380 4438	ValArgAsnPheLysValSerAsnThrGlnAspAlaSerValSerIleValAspTyrTy 	LysLeuAsnLeuTyrLeuAspSerValAsnGluThrGlnPheCysValAsnIleProAla ::: ::	GluAlaIleSerLeuSerGluThrValLysLysValGluTyrAspHisGly	ArgSerGlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSer	AspLeuAsnHisValAspLeuAsnValCysThrSerPheSerGlyProGly	InAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLysAsp 	GlnLeuAsnValValTyrAsnValLysAlaSerGlySerSerArgArgArgArgArgSerIle :::::: :::
				T 1368	a 1348 T 4342	y 1328 C 4282	r 1311 G 4222	- 1292 C 4162	p 1275 T 4102	e 1258 : C 4042

317 SerProGlyProValGluIleLeuThrThrValThrGluSerVal 331	GluGluMetLysAsnValMetAspSerSerAsnGlyLeuSerGluTyrLeuAspLeuSer	277 LysLysAsnIleThrLysThrPheLysIleAsnGlyScrAlaAsnPheScrPheAsnAsp 296 277 LysLysAsnIleThrLysThrPheLysIleAsnGlyScrAlaAsnPheScrPheAsnAsp 296	SerPheTrpGlyLys		244 LysHisLeuAsnGlyThrIleThrAlaLysTyrThrTyrGlyLysProValLysGlyAsp 263 ::: ::: ::::::		206 IleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGlnValSerGlu 223 ::: 686 GTGGTGGTACAGAAATCAGGTGGAAGGACAGAGCACCCTTTCACCGTGGAGGAA 742	186 LeuGlyVallleSerLysThrPheGlnLeuSerSerHisProIleLeuGlyAspTrpSer 205	167 LeuIleLysAspProLysSerAsnLeuIleGlnGlnTrpLeuSerGlnGlnSerAsp 185 ::: ::: ::: 566 GTATACATTCAGGATCCCAAAGGAAATCGCATCGCACAATGGCAGAGTTTCCAGTTAGAG 625	147 LysPheArgIleValThrLeuPheSerAspPheLysProTyrLysThrSerLeuAsnIle 166		107 ThrGlyArgThrGlnAspGluIleLeuPheSerAsnSerThrArgLeuSerPheGluThr 126	90 LeuProSerLeuProLeuAsnSerAlaAspGluIleTyrGluLeuArgVal 106 :::::: :::: 341GCTGTCCCAAGTCTTCATCCAATGAGGAGGTAATGTTCCTCACTGTCCAAGTG 394	72SerValLeuGluAlaGluGlyValPheGluLysGlySerPheLysThrLeuThr 89 :::	52 CysProSerGlnValThrValLysAlaGluLeuLeuLysThrAlaSerAsnLeuThrVal 71	32 AlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeuGluHis 51	12 LeuLeuCysValCysThrAlaAlaLeuAlaValAlaProGlyProArgPheLeuValThr 31 116 CTCTTGGTCCTGCCCACAGACGCCTCAGTCTCTGGAAAACCGCAGTATATGGTTCTG 175
Qy -632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651 Qy -632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651 Qy -632 ValPheGlnGluCysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIle 651	620 GlyTyrTyrLeuGlyMet	Qy 601 AlaSerAsnAspIleThrMetGluAsnValValHisGluLeuGluLeuTyrAsnThr 619	Qy 581 ThrGlnProAspSerIleValGlyIleValAlaValAspLysSerValAsnLeuMetAsn 600	Qy 561 LeuTyrTrpSerLysValLysAlaGluProSerGluLysValSerLeuArgIleSerVal 580	Qy 541 GluileileSerAspValLeuLysileProValGlnLeuValPheLysAsnLysileLys 560	Qy 521 ProGluAsnSerTrpThrProLysAlaCysValIleValTyrTyrIleGluAspAspGly 540	Qy 511	Qy 493 LeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGly 510 :::	Qy 479 ValGlySerProPheGluLeuValValSerGlyAsnLysArg 492	459 LeuPheLysSerProSerLy	Qy 439 SerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLysSerSerMetAlaValHisSer 458	Qy 429 LyslleGluPhePro	Qy 412 MetGluAlaValGlnLysIleAsnTyrThrValProGlnSerGlyThrPhe 428	Db 1226 TTCATCAGAGGAAATGAAGCAAACTATTACTCCAATGCTACCACGGATGAG 1276	372 VAITHTATGALAASPGIJAASHGILHEUTHTEUGLUGIUAZGATGASHASHVALVALIIe	352 GLUPhePheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLys	:::

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ACCAGTGGAAGGCACTTCTGCCTGTCTGAAGATGCTGGACTTGGTATCTTCTCCTC ThrProValGluLeuGInAlaPheGInFroPheFheIlePheIleProTyTSer	2078 TTCCTAGAGGACATGGGCTTAAAGGCATTCACCAAACTCCAAAGATTCGTAAACCCAAAATG 2137 652 AspGlyValTyrAspAsnAlaGluTyr 660 2138 TGTCCACAGCTTCAACAGTATGAATGCACTGAAGGTCTACGTGTAGGTTTTTAT 2197 661 AlaGluArgPheMetGluGluAsnGluGlyHis1leValAspIleHisAspPheSerLeu 680 2198 GAGTCAGATGTAATGGGAAGAGGCCATGCACGCCTGGTGCATGTTGAAGAG 2248 681 GlySerSerProHisValArgLysHisPheProGluThrTTpIleTrpLeu 697 2249CCTCACAGGAGACCGTACGAAAGTACTTCCCTGAGACATGGATCTGGGAT 2299 698 AspThrAsnMetGlyTyrArgIleTyrGlnGluPheGluValThrValProAspSerIle 717 2300 TTGGTGGTGGTGAAACTCAGCAGGTGGGCTGAGGAGAGAGGTAACAGTCCCTGACACCATC 2359 718 ThrSerTrpValAlaThrClyPheValIleSerGTAAGGTAAGAGTCCCTGACACCATC 2359
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1075 INCICITICIGAGATTCCTCTCACAGTCACTGATCCCTGTTTGC 3454 1075	977 PheGlyAsnTyrAspProSerGlySerThrTrpLeuSerAlaPheValLeuArg 994

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US-09-756-247-3
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                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
SEQ ID NO 3
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS
TITLE OF INVENTION: AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-31CIP
                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo
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     LeuAlaValAlaProGly-----
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Tang, Y. Tom
Liu, Chenghua
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Goodrich, Ryle
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Mize, Nancy K
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                                                       976 GAGGCCAATGCCACTCAGAATATCTACATTTCTCCACAAATGGGATCAATGACCTTTGAA 1038
                                                                                                                                                                                                 856 ACTGACAAAACAGGATGTTTCTCAGCACCTGTGGACATGGCCACCTTTGACCTCATTGGA
                                                                                                                                                                                                                                   313 LeuAsp-----LeuSerSerPro-----
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AspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLysValThrArg
                                                                                                                                                                                                                                                                                                                                                                                                                                           LysTyrThrTyrGlyLysProValLysGlyAspValThrLeuThrPheLeuProLeuSer 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LeuGlnThrProLeuTyrCysSerMetAsnSerLysHisLeuAsnGlyThrIleThrAla
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                                                                                     SerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhePhe
                                                                                                                                                              -----GlyProValGluIleLeuThrThrValThrGluSerValThrGlyIle
                                                                                                                                                                                                                                                                                                                                                                               PheTrpGlyLysLysLysAsnIleThrLysThrPheLysIleAsnGlySerAlaAsnPhe 292
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	1036 GACACCAGCAATTTTTACCATCCAAATTTCCCCTTCAGTGGAAAGATAAGAGTTAGGGGC 1095 375 AlaaspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIle391
Db 2305 ACTTCCCAGTCAMAGGCTTCGGGCTTTCACCCACTGTTGGACTAACTGCTTTCAMG 2361 Qy 747 PAPPhePheIlePheILeLMSHILEWPSCYTAISEXTAILLARYGGIYGIUGIUADHAALAEW 766	636 CysGlyLeuTrpValLeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyr

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1243 4005	1224 MetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValVal:::	
1223 3945	1211GlyProSerSerProSerProLeuAlaValGln	
1210 3885	AGAATTTCCAGCGCACA	
1196 3825	179 AlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAla :::	ωμ
1178 3765	Phe	ωμ
1158 3705	1144 ValalaalaTyralaLeuLeuSerHis	
1143 3645	GlnProArgSerLeuAspIleGlu TCTGAGCCTGCGGCTGTAGATGTGGAA	
1126 3585	1107 AlaLeuAsnMetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpVal8er	ωµ
1106 3525	1088 ThrLeuAlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGlu	
1087 3465	1068 ValGlnGluSerIleHisPheLeuGluSerGluPheSerArgGlyIleSerAspAsnTyr	ω μ
1067 3408	1048 LeuThrAlaTyrIleValThrSerLeuLeuGlyTyrArgLysTyrGlnProAsnIleAsp	
1047 3348	1028 TrpAspProGlyArgVallleHisSerGluLeuGlnGlyGlyAsnLyBSerProValThr	
1027 3288	1008 AsnValLeuHisArgThrTyrThrTrpLeuLysGlyHisGlnLysSerAsnGlyGluPhe ::: :: :: :: :: :: :: :: :: :: :: :: :: :: ::	
1007 3228	988 LeuSerAlaPheValLeuArgCysPheLeuGluAlaAspProTyrIleAspIleAspGln ::: 	
987 3168	968 GlnArgGluAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGlySerThrTrp :::	
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVDGSQKARLDVIGDMMGPVLNNAHKLVQMPYGCGEQNMLNLVPNILVVKYLRATNRNES
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                                          TOFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRP 1398
                                                                                      CCNYTRPGKSNMALABIDALSGYRFDAEQVHTLTSIEDLQRVEMEKDDTKMNVYFNPLGG
                                                                                                                                                                               AVSINANGTGVVFAQLSYSY------YRDSLNDDAPFFCSQEIKEIRAG-NRLQLDL
                                                                                                                                                                                                                                   AVNISANGEGEAI COLNVVYNVKASGSSRRRRSI ONQEAEDLDVAVKENKDDLNHVDLNV
                                                                                                                                                                                                                                                                                  TSTQDTVMALQALSSYAAVTYSDKHTSQVTILNGKHTHSFDINIRNAIVLQSYQLSSLND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVQESIHFLESEFSRGISDNYTLALITYALSSVGSPKAKEALNMLTWR--AEQEGGMQFW 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QLETKAIKFIEQGIQRELTYKRADNSFSAFGDSDKAGSTWLTAFVVRSFHHAKQYAFVDP 1070
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                                                                                                                                   CTSFSGPGRSGMALMEVNILLSGFMVPSEAISLSETVK----KVEYDHGKLNLYLDSVNE
                                                                                                                                                                                                                                                                                                                                                                                SAQKKVEKLKESRAYMFQARPVDIETTSYAVLSYLAQNQTSESLSIIRWLVSQRNELGGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVISRAVAFLNSQQMESGAFAERGEVHHKDMQGGAQDGGVALTAFVLISIL----ENGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVLHRTYTWLKGHQKSNGEFWDPGRVIHSELQGG-NKSPVTLTAYIVTSLLGYRKYQPNI 1066
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGKAVTYLEKHLDEVSGNAYTMAVVAYALQLAKSKQAGKAFENLKKHKI VEKSGDVKFA
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A;Residues: 1-1519 <WIL>
A;Cross-references: EMBL:Z82090; PIDN:CAB05007.1; GSPDB:GN00019; CESP:ZK337.1b
A;Experimental source: clone ZK337
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
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Typothetical protein ZK337.1b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T27829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 1
A;Introns: 36/2; 116/3; 201/1; 267/2; 338/3; 413/3; 527/3; 556/3; 691/3; 714/1; 771/2; C;Superfamily: alpha-2-macroglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library
A;Reference number: Z20426
A;Accession: T27829
A;Status: preliminary; translated
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RESULT 3
T18544
alpha-2-macroglobulin - Limulus sp.
C;Species: Limulus sp.
C;Species: Limulus sp.
C;Ate: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 15-Sep-2000
C;Accession: T18544
R;Iwakki, D.; Kawabata, S.; Miura, Y.; Kato, A.; Armstrong, P.B.; Quigley, J.P.; N
Eur. J. Biochem. 242, 822-831, 1996
A;Title: Molecular cloning of Limulus alpha-2-macroglobulin.
A;Reference number: Z18961; MUID:97175055; PMID:9022715
A;Accession: T18544
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecular type: mRNA
A;Residues: 1-1507 < IWA>
A;Cross-references: EMBL:D83196; NID:d1096438; PID:d1020631; PIDN:BAA19844.1
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                                                                                                                                    CISEETGLGVSEA-ATVKGFQPFFVSFTLPYSVIRGEKVPIIVTVFNYLSECLPIKLSLE
                                                                                                                                                       VISEDLGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIE
                                                                                                                                                                                                       GEAGGFGGGIRKKTNKPVVBIRTYFPETWLWBLQNIGATGELSLKRDIPHTITEWVGSAI
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                                                             QSDKF-----
                                                                                               KSDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALS-----
                                                                                                                                                                                                                                                                                STNYLDSITAFDEAGLVVISDMELETRPCKPSGFEDGGRPCPQYDVAFAAPQAANRIGGG
                                                                                                                                                                                                                                                                                                                LGMFMNSFAVFQECGLWVLTDANL-----TKDYIDGVYDNAEYAERFMEENEGHIV---
                                                                                                                                                                                                                                                                                                                                                                                       KSVNLMNASNDITMENVVHEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            YYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSKTYIQLKTRDENIKVGSPFEL---VVSGNKRLKELSYMVVSRGQLVAVGK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKE--FTSDEAGIIKFTVPPQTPDITSFRFKAKALQYGKKDGDNKLNQPQHSFTVSSWYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VQKINYTVPQSGTFKIEF-PILEDSSELQLKAYFL-----GSKSSMAVHSL----FKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGKGYLKPGLPFYGKLKVEKPDGTPAPGEQ-----IELCRFADRERWNRKRWLEEKIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T---VLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFIQTDKALYKPKQEVKFRIVTLESDFK--PYKTSLNILIKDPKSNLIQQWLSQQSDLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SFNKDNPSSSIQLTIPSGVEVKRPKLYANGSY----SSPSSNDFFFEKD--INMHKDKLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILTAPKSLTPGKSNILNLHLFD-
                                                                                                                                                                                                                                         -DIHDFSLG-----SSP--HVRKHFPETWIWLDTWMGYRIYQEFEVTVPDSITSWVATGF
                                                                                                                                                                                                                                                                                                                                                    KSVHILSSDNRITEEEVFNKLGGHDYYWPKQATSDYKYCEDYKFKQTEGEHEGSFSSGFT
                                                                                                                                                                                                                                                                                                                                                                                                                           FYVREDGETVADSTKITVKKCLRNKVGLKFGEEKVLPGASSTLQLTAS-PYSICGIGAVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDKSGLTDETYLPIDVTALSLNPPNEPEWENNVIVPPHIGETSLTLIPSFEMNPSAKILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----QNSTMFSLTPEN--SW----------TPKACVIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSGSHLQLEPITEEIECGKPLTVKFKYTTGEEKKQKFYYQIMARNFIVDTGSFEHEFLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative 270;
       - PTASDAVTOMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.3%;
                                                               EMONDTNSYTSCVCGGKSDTTRWMIKPRSLGQVNLTVYGASLPNEAIC
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Pred. No. 1.3e-84;
70; Mismatches 559
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785 882 838 935 823

725

464 464 511 524 533 584 593 593 593 643 703 190

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A;Molecule type: mRNA
A;Residues: 1-1476 <IWA>
A;Residues: 1-1476 <IWA>
A;Cross-references: DDBJ:D84338; NID:g1805591; PIDN:BAA12316.1; PID:g1304084
C;Comment: This protein belongs to alpha 2-macroglobulin family.
C;Superfamily: alpha-2-macroglobulin
C;Superfamily: alpha-2-macroglobulin
F;1-23/Domain: signal sequence #status predicted <SIG>
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JC5143
                                                                                                                                                                                                                                                                                                                                                                                                              R.Iwasaki, H.; Suzuki, Y.; Sinohara, H.
J. Biochem. 120, 1167-1175, 1996
A.;Title: Cloning and sequencing of cDNAs encoding plasma
A.Reference number: JC5143; MUID:97164019; PMID:9010766
A.;Contents: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alpha-macroglobulin precursor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-dan-1997 #sequence_revision 27-Feb-1997
C;Accession: JC5143
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A;Status: preliminary
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Best Local Similarity
Matches 451; Conserv
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LSFETKRISVF1QTDKALYKPKQEVKFRIVTLFSDFKPYKTSLN-----ILIKDPKSNLI 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIRENGSLFMNMVAEKDLFQCVAF---TVPQSPYPEAVMFLTVEVEGPTHG---FRSRKT 119
                                                                                                                            PVLL----LIILAADASISGKPQYMVLVPSLLHSGTPEKICL-LLTQLNETVTVKASLD
                                                                                                                                                      PPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAEL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YFSELTDQNLCFNFWLEQDIEVQETKPATIRLYDYYELEQEVVTSYSID---ENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -AHIATCVKYDGKGGVSNMAVLEMKMVSGWIPDEESIKNIVDREELNLRRYEVDGNQLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HVDLNVCTSFSGPGR-SGMALMEVNLLSGFMVPSEAIS-----LSETVKKVEYDHGKLNL 1332
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                                                                                         -LKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCD 1388
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                                                                                                                                                                                                20.3%; Score 1491; DB 2; Length 1.
28.8%; Pred. No. 2.8e-76;
tive 292; Mismatches 524; Indels
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                                                                                                                                                                                                                                  Length 1476;
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                                                                                                                                                                                                                     ATVSILGDILGSAMQNIQNLLQMPYGCGEQNMVLFAPNIYVLDYLNETQQLTPDIKSKAI
                                                                                                                                                                                                                                      VQITAIGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKAL:::||:|| :: ||:|| :: ||:|| :: ||:||
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EANEGASHTANAVFSL----SRSFVHLEPQLGKLPCHQTQTFKA----HYILKG-QELKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ITITASEANY-----HSNATTDENGLVQFSINTTNMIGTSLNIQVKHKDSTNCYDYQWLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESVTGISRNVSTNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SAN-----FSFNDEEMK-------NVMDSSNGLSEYLDLSSPGPVEILTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOWQNLKLERGLTQLSFPLSSEPLLGSYSVVVHKESGGRMHHSFTVEEFVLPKFEVQVSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLVKSKDSLVFVQTDKPIYKPGQTVKARVVSLDENFRP----LNELFPLIFIQDPKGNRV
   FCLESAWKSAKEGTHG-SHVYTKALLAYAFALAGNQERKKEILKSLEDEGVKEDNSLHWA
                                      HFLES----
                                                                          ALSWLSQKQKDNGCFWSSGSLLNNAIKGGVEDEISLSÄYITIALLEMSLPDTHPVVRNAL
                                                                                                         TYTWLKGHOKSNGEFWDPGRVIHSELOGGNKSPVTLTAYIVTSLLGYRKYOPNIDVQESI
                                                                                                                                            SYLSTGYQRQLNYKHRDGSYSTFGENYRGGQGNTWLTAFVLKTFSQARKYIFIDEAHITQ
                                                                                                                                                               SFMRQGYQRELLYQREDGSFSAFG-NY-DPSGSTWLSAFVLRCFLEADPYIDIDQNVLHR
                                                                                                                                                                                                                                                                                                                           LSPT--ASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSER
                                                                                                                                                                                                                                                                                                                                                              LAEPKAKE-----QESYCVCGNERQTVSWVVTPKSLGNVNFTVSAEALESSELCGNEKT
                                                                                                                                                                                                                                                                                                                                                                                                 DILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTA------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAATYSEPPKETVRTYSPETWIWDLKVTDSSG---VAEVEVTVPDTITEWKAGAFCLSND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----VRKHFPETWIW---LDTNMGYRIYQEFEVTVPDSITSWVATGFVISED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLKDMGLKVFTNTKIQKPQLCAHVQKFEVPTMAYSYSESS-----SFRSGPRRVPAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFQECGLWVLTDANLTKDYIDGVYDNAEYAERFMEENEGHIVDIHDFSLGSSPH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLSASSVYALLPVKDLTGFPGLLGQQEENDGECVSLYNT-YIDGILYSPEPNINEKDMYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L--SYMVVSRGQLVAVG-----KQNST----MFSLTPENSWTPKACVIVYYIEDDGEII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAYFLGSKSSMAVHSLFKSPSKTYIQLKT-----RDENIKVGSPFELVVSGNKRLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLNSQGCFIQQVKTNDFQLRRKEYEMRLRVEAKIREEGTG----VQLTGTGFSEITATIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKKITILEQEFTVSVCGRYTYGKPVPGNITMSICRNYNNPSACLSEE---SRAFCKKYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OOMISOOSDIGAISKIEGISSHEIIGDMSIOA-OANDOLLAKSEAATSEAATSEALIOL
                             EFSRGISDNYTLALITYALSSVGS-PKAKEALNMLTWRAEQEGGMQFWV
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Query Match Best Local Similarity 29.4%; Pred. No. 3.1e-74; Matches 457; Conservative 237; Mismatches 578; Indels 284; Gaps 50; Qy 13 LCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASN 68 :: : : : Db 9 LCLFSALLAFLPFASILNGNSKYMVLPSQLYTETPEKICHLYHLNETVT 59 Qy 69 LTVSVLEAEGVFEKGSFKTLTLPSLPINSADETYELTGRTQDETLFSN 118 : : : : : : : : : Db 60 VTASLISQRGTRKLFDELVVDKDLFHCVSFTIPRLPSSEEEESLDINIEGAKHKFSE 116	R;Enghild, J.J.; Salvesen, G; Thogersen, I.B.; Pizzo, S.V. J. Biol. Chem. 264, 11428-11435, 1989 A;Title: Proteinase binding and inhibition by the monomeric alpha-macroglobulin rat alph A;Reference number: A34278; MUID:89291900; PMID:2472396 A;Accession: A34278 A;Molecule type: protein A;Residues: 673-676,'T',678-723 <eng> C;Superfamily: alpha-2-macroglobulin F;1-24/Domain: signal sequence #status predicted <sig> F;25-1477/Product: alpha-1-inhibitor III #status predicted <mat></mat></sig></eng>	BB:J03552; NID:g202571; BB:J03552; NID:g202571; bayashi, K.; Geiger, T 375-381, 1987 on and sequencing of c (27199; MUID:87190405; c27199; NID:g204930; BB:M28297; NID:g204930;	RESULT 5 A2952 A2952 alpha-1 proteinase inhibitor III precursor - rat C;Species: Rattus morvegicus (Norway rat) C;Date: 19-Nov-1988 #sequence revision 19-Nov-1988 #text_change 16-Jul-1999 C;Accession: A29952; A27199; Ā34278 R;Braciak, T.A.; Northemann, W.; Hudson, G.O.; Shiels, B.R.; Gehring, M.R.; Fey, G.H. J. Biol. Chem. 263, 3999-4012, 1988 A;Title: Sequence and acute phase regulation of rat alpha-1-inhibitor III messenger RNA. A;Reference number: A92709; MUID:88153707; PMID:2831216 A;Molecule type: mRNA. A;Molecule type: mRNA	Db 1401 LEKSEHISKNEIDHSKLHLINDSVNEIGECVELPAKREKVENTGDASYSLVDYYEPRKQ 13/3 Db 1401 LEKSEHISRTEVSNNHVLIYLDKVSNQTLSLSFFVVQDIEVRDLKPAIIKVYDYYETNEF 1460 Qy 1374 AVRSYNS 1380	1126 SSES-KLSDSWQPRSLDIEVAAYALLSHFLQFQTSEGIPIMRWLSR 1
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901 GDVLGPSINGLASLIRMPYGCGEQNMINEAPNIYILDYLTKKKOLTDNLKEKALSFYRGG 960	785 SV-ASFQAFQPFFVELIMPYSVIRGEAFTLKATVLNYLPTSLPMAVLLEASPDF	641 LTDANL-TKDYIDGVYDNAEYA	491 KRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIED 538	331 SEFSGSRIEVERTRNKFUFLKADSHFRHGIPFFVKVRLVDIKGDPIPNEQVLIKA 386 394 TQRNYTEYWSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSS 453 397 RDAGYTNATTTDQHGLAKFSIDTNGISDYS-LNIKVYHKEES 427 387 RDAGYTNATTTDQHGLAKFSIDTNGISDYS-LNIKVYHKEES 427 454 MAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGN 490 1 1 1 1 1 1 1 1 1 1	117 RRVVIVKNKESVVEVQTDKEMYKPOQSVKERVVSMDKNLHPLNELFPLAYIEDEKM 172 174 NLIQOMLSQOSDLGVISKTEQLSSHPILGDWSIQVQVNDQTYYQSEQVSEYVLPKF 229

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R;Kan, c...
Natl. /
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A;Residues: 672-747 <MAR>
A;Residues: 672-747 <MAR>
R;Matthijs, G.; Devriendt, K.; Cassiman, J.J.; Van Den Berghe,
Biochem. Biophys. Res. Commun. 184, 596-603, 1992
A;Title: Structure of the human alpha-2 macroglobulin gene and
A;Reference number: JN0262; MUID:92246939; PMID:1374237
A;Accession: JN0262
                                                                                          A;Residues: 1-29 <MAT>
R;Sottrup-Jensen, L.; Stepanik, T.M.; Kristensen, T.; Wier: J. Biol. Chem. 259, 8318-8327, 1984
A;Title: Primary structure of human alpha-2-macroglobulin. A;Reference number: A92486; MUID:84239807; PMID:6203908
                                                                                                                                                                                                            A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-29 <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 832-999, 'I', 1001-1147, 'D', 1149-1194, 'D', 1196-1474 <BEL>
A; Cross-references: GB: M36501; NID: g177871; PIDN: AAA51552.1; PID: g177872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 05-Apr-1983 #sequence revision 30-Jun-1987 #text change 08-Dec-2000
C;Date: 05-Apr-1983 #s9375; S09107; JN0262; A92486; S66634; A01256
C;Accession: A94033; 1393975; S09107; JN0262; A92486; S66634; A01256
R;Kan, C.C.; Solomon, B.; Belt, K.T.; Chain, A.C.; Hiorns, L.R.; Fey, G.
Proc. Natl. Acad. Sci. U.S.A. 82, 2282-2286, 1985
A;Title: Nucleotide sequence of cDNA encoding human alpha-2-macroglobulin and A;Reference number: A94033; MUID:85190481; PMID:2581245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Marynen, P.; Devriendt, K.; van den Berghe, FEBS Lett. 262, 349-352, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Somat. Cell Mol. Genet. 11, 285-289, 1985
A;Title: Human alpha 2-macroglobulin gene is located on A;Reference number: I39375; MUID:85219061; PMID:2408344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Bell, G.I.; Rall, L.B.; Sanchez-Pescador, R.; Merryweather, J.P.; Scott, Somat. Cell Mol. Genet. 11, 285-289, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mkNA
A; Residues: 1-1474 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: S09106;
A;Accession: S09107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M11313; NID:g177869; PIDN:AAA51551.1; PID:g177870
A;Note: hydrolysis of the thiolester bond during amino acid sequencing o
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N;Alternate names: alpha-2M
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,Molecule type: protein
;Residues: 24-562,'E',564-974,'Z',976-999,'I',1001-1474 <50T>
                                                                     Accession: A92486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MUID:90242963;
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125 186 185

GGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEH-PFTVEEFVLPKFEVQVTVPKIITILE

243 243

EDSLVFVQTĎKSIYKÞGQTVKFRVVSMDENĖHÞLNELIFLVYĬQĎÞKGNRÍAQMQSFQLE 184 LĠVISKTFQLSSHÞILĠDWSIQVQND--QTYYQSFQVSBYVLÞKFBVTLQTÞLYCSMNS 243

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A; Molecule type: protein
A; Residues: 1337-1343 cDCl>
C; Comment: This inits receptor-specific binding site.
C; comment: The entrapped enzyme remains active against low molecular weight substrates (&C; comment: The entrapped enzyme remains active against low molecular weight substrates (&C; comment: The wide specificity of this inhibitor is attributed to the primary sequence (c); comment: The wide specificity of this inhibitor is attributed to the primary sequence (c); this of a variety of plasma proteinases, form primary (residues 704-809) and secondary (c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-1474/Product: alpha-2-macroglobin #status experimental <MA2>
F;693-694,704-709,719-723,730-735/Region: inhibitory #status predicted
F;698-742/Region: bait region
F;698-742/Region: bait region
F;498-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-431,595-771,642-689,821-849,847-883,921-1321,1079-1127,1352-:
F;48-86,251-299,269-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-287,278-2
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A;Title: Crystallisation and preliminary X-ray analysis of the re A;Reference number: S66634; MUID:96032553; PMID:7556651
A;Accession: S66634
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R;Hall, P.K.; Nelles, L.P.; Travis, J.; Roberts, R.C.
Biochem. Biophys. Res. Commun. 100, 8-16, 1981
A;Title: Proteolytic cleavage sites on alpha-2-macroglobulin resulting in
A;Reference number: A90099; MUID:8125805; PMID:6167263
A;Contents: annotation; inhibitory site
R;Mortensen, S.B.; Sottrup-Jensen, L.; Hansen, H.F.; Petersen, T.E.; Magnu
REBS Lett. 135, 295-300, 1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:119639; OMIM:103950
A;Map position: 12p13.3-12p12.3
C;Complex: homotetramer; dimer of disulfide linked dimers
C;Superfamily: alpha-2-macroglobulin
C;Keywords: glycoprotein; plasma; proteinase inhibitor; thiolester
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Hoppe-Seyler's Z. Physiol. Chem. 364, 1297-1302, 1983
A;Title: Human neutrophil elastase and cathepsin G cleavage
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. Biol. Chem. 260, 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 451;
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FTDLEAENDVLHCVAF-----AVPKSSSNEEVMFLTVQVKGPTQE---FKKRTTVMVKN 124
                                                                                                                                                                                                 -SVLEAEG-VFEKGSFKTLTLPSLPLNSADE---IYELRVTGRTQDEILFSNSTRLSFET
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167-173, 1981
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1440; DB 1;
Pred. No. 2.2e-73;
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Q I	1125 VSSESKLSDSWQPRSLDIEVAAYALLSHFLQFQTSEGIPIMRWLSRQRNSL 1175 ::::: :: : : : :: :: :: :: :: ::
라 ઇ	1075 LESEFSRGISDNYTLALITYALSSVGS-PKAKEALNWLTWRAEQEGGMQFW 1124
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j 2 8	842SDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPDNTVTGSERVQ 896
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B 8 8	738 TPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSS 797
F & ;	681 GSSPHVRKHPPETWIWLDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTT 737 : :: :::
S W S	632 VFQECGLWVLTDANLTKDYIDGVYDNAEYAERFMEENEGHIVDIHDFSL 680
7 A A A ;	601 ASNDITMENVVHEL-ELYNTGYYLGMFMNSFA 631
A; R A; S A; St	541 EIISDYLKIPVQLVFKNKIKLYMSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLAN 600
N C C C	493 LKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDG 540 : :::: :::
RESI T43: alpl	439 SELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKR 492
Db 45	392 TVTQRNYTEYWSGSNSGNQKMEAVQ-KINYTVPQSGTFKIEFPILEDS 438 :
S B &	332 TGISRNVSTNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVI 391
) D &	277 KKNITKTEKINGSANFSENDEEMKNVMDSSNGLSEYLDLSSPGFVEILTTVTESV 331 ::
D D S	244 KHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGK 276
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Reference number: Z22323
Accession: T43166
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
Residues: 1-1503 <NON>
Cross-references: EMBL:D13567; PIDN:BAA02762.1
Experimental source: liver; clone Cl.3 and Cl1.10
Superfamily: alpha-2-macroglobulin
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19.4%; Score 1424; DB 2;
Best Local Similarity 28.3%; Pred. No. 1.8e-72;
Matches 442; Conservative 256; Mismatches 600;
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Species: Lampetra japonica (Japanese lamprey)
Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 20-Jun-2000
Accession: T43166
Nonaka, M.
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GYSTISAFFSPSDSFLQLDRVAHTLECGSSVPLRLLLV----LKENRSSAGDGHAGGVVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NLIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQV---QVNDQTYYQSFQVSEYVLPKFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LFSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKP-YKTSLNILIKDPKS
                                            SMAVHSLFKSPSKTYIQLKTRDENIKVGS--PFELVVSGNKRLKE----
                                                                                              GNAAPPGSQHHTG----ADGTFTFTI-DTGDFNRSDTIFLEATDPEFNSTAHPSVTYQQ
                                                                                                                                                                                                                                          RNVSTNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQ
                                                                                                                                                                                                                                                                                                                                      NFSFNDEEMKNVMD-----SSNGLSEY-LDLSSPG-----PVEILTTVTESVTGIS
                                                                                                                                                                                                                                                                                                                                                                                      VSIQTPSYLNYLDKSVTLKVCGRYTYGKPVHGAVNASVC----
                                                                                                                                                                                                                                                                                                                                                                                                                                     VTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRIAQWRNASGRAGIVQLELDMPSEPPLGTYNVMVVEQSGGDSVASHTFTVEEYVLPTFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSRDTSHVAQNHTVVGEVDAGVLLQPSGGDLHHCFSFTVP-DVQGTTYANLVVRAAGEGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNS 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS 1304
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                                                                                                                                                                                           MKQKAEKNFETDITRISFVDMPSWYRHGLPIVGKVKVERPDGSPVP----HKLVSLIVKQ
                                                                                                                                                                                                                                                                                         REWWREECIIPVCNEFEMKVGKDGCAEWQVDNAKPSNASCHTTHVLKVVAVLEEEGTGMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASNITVSVIEAEGVFEKGSFKTLTLPS-----LPLNSADEIYELRVTGRTQDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AFLILLCALAAVVSADEQSSGHYLVFVPSELHALSSERLCVSLL-GVTGEVTFRATLHYK
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                                          SYNS 1380
                                                                                        YDFVKKVEVDASRVVIYLDKVDKKPIAIKLSVTQDIAVDNLQPATVRVYDYYATEDAATS
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                                                                                                                                                                                SLSVETNPANCSKAARKGFQINVEVSYHGERGESNMALVEVKMISGYSAVKSSLKELQTF
                                                                                                                                                                                                                                                                        NALILHQVQLPPPVPAPMVSSCTVEATGQGCALFQVSLKYNEPPKSSKPK-----F
                                                                                                                                                                                                                                                                                                                   SS-----PSPLAVVQPMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QK-SNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNID----VQESIH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQRQLTYKRDDHSYSAFGKSDDDGNTWLTAFVLKSFVRASKHIAVSEDHITGPFSWLVEH
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                                                                                                                                   ---VKKVEYDHGKLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVR
                                                                                                                                                                                                                                                                                                                                                                   QRNAYGGFSSTQDTVVGLQALSAFAALIDGDGGGGGGGGKAVVLDSAHTLLREVSIDST
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Alpha-1 proteinase inhibitor III, variant 1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text_change 16-Jul-1999
C;Cacession: S15904; SS2235; \overline{\overline{S}}29737; B34278; B29952; C29\overline{S}22; D29952; B27199
R;Regler, R; Sickinger, S.; Schweizer, M.
FBBS Lett. 202, 368-372, 1991
A;Title: Differential regulation of the two mRNA species of the rodent negat
A;Reference number: S15904; MUID:91243832; PMID:1709877
A;Introns: 29/2; 90/3; 144/1
C;Superfamily: alpha-2-macroglobulin
C;Keywords: proteinase inhibitor; thiolester bond
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1487/Product: alpha-1 inhibitor III variant 1 #status predicted <MAT>
F;648-723/Region: bait region #status predicted
F;985-988/Cross-link: thiolester (Cys-Gln) #status predicted
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A; Residues: 684-715,'N','11-733 <ENG>
R; Braciak, T.A.; Northemann, W.; Hudson, G.O.; Shiels, B.R.; Gehring,
R; Braciak, T.A.; Northemann, 1988
J; Biol. Chem. 263, 3999-4012, 1988
A; Title: Sequence and acute phase regulation of rat alpha-1-inhibitor
A; Reference number: A92709; MUID:88153707; PMID:2831216
A; Accession: B29952
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J. Biol. Chem. 264, 11428-11435, 1989
A;Fitle: Proteinase binding and inhibition by the monomeric alpha-macroglobulin rat alpha, Reference number: 34278; MUID:89291900; PMID:2472396
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Eur. J. Blochem. 164, 375-381, 1987
A;Tille: Identification and sequencing of cDNA clones for the
A;Reference number: A27199; MUID:87190405; PMID:2436907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 315-409;1064-1079,'LAASGAPDHC',1090,'TMP'
A;Cross-references: GB:M22361; GB:M22362
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A;Title: alpha-macroglobulin domain structure studied by A;Reference number: S29737; MUID:93143334; PMID:7678727
A;Accession: S29737
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A; Residues: 1416-1483, 'N', 1485-1487 <SCH>
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A;Cross-references: GB:M22360; NID:g202583;
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A; Residues: 1-161 <SIC>
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A; Residues: 1-1487 < REG>
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A;Molecule type: DNA
A;Residues: 1-146 <RES>
A;Residues: 1-146 <RES>
A;Cross-references: GB:M23567; NID:g202598; PIDN:AAA77658.1; PID:g554404
A;Cross-references: GB:M23567; NID:g202598; PIDN:AAA77658.1; PID:g554404
R;Tsuchiya, Y: Hattori, M.; Hayashida, K.; Ishibashi, H.; Okubo, H.; Sakaki, Gene 57, 73-80, 1987
Gene 57, 73-80, 1987
A;Title: Sequence analysis of the putative regulatory region of rat alpha-2-m:A;Reference number: I54013; MUID:88112864; PMID:2448189
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A;Title: Molecular cloning of cDNA sequences for rat alpha-2-macroglobulin and A;Reference number: A22614; MUID:85207604; PMID:2581948
A;Accession: A22614
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A;Molecule type: DNA
A;Residues: 1-23,'A',25-227 <RE2>
A;Cross-references: GB:M22670; NID:g205388; PIDN:AAA41592.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: the authors translated the codon ATT for residue R;Northemann, W.; Shiels, B.R.; Braciak, T.A.; Hanson, R. Biochemistry 27, 9194-9203, 1984. A;Tile: Structure and acute-phase regulation of the rat A;Reference number: I52403; MUID:89207509; PMID:2468362 A;Accession: I52403
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                              TORNYTEYWSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILED---SSELQLKAYF---
                                                                                                                              CFSQLVKTKSFQLK-RQEYEMQLDVHAKIQEEGTGVEE----TGKG----LTKITRTITK
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                                                                                             ISRNVSTNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITV
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                                                                                                                                                              TKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVBILTTVTESVTG
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-EANLYINTTTDKHGLAR--FSINTDDIMGTSLTVRAKYKDS
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.W.; Heinrich,
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                                                                  SFOISLNISYTGSRSESNMAIADVKMVSGFIPLKPTVKMLERSVHVSRTEVSNNHVLIYL
                                                                                                                          DLNVCTSFSGPG---RSGMALMEVNLLSGFMVPSEAISLSET---VKKVEYDHGKLNLYL
                                                                                                                                                                                            DYTVKVTGEGCVYLQTSLKYSV------LPREEEFPFAVVVQTLPGTCEDPKAHT
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Qy 496 LSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDGE 541 : : ::		Query Match 19.1%; Score 1402; DB 2; Length 1451; Best Local Similarity 27.7%; Pred. No. 3.1e-71; Matches 439; Conservative 250; Mismatches 527; Indels 370; Gaps 54; Qy 13 LCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKT 65 :: :: : :: :: :: : :	RESULT 10 B41185 alpha-2 macroglobulin homolog MUG2 - mouse C;Species: Mus muscullus (house mouse) C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 16-Jul-1999 C;Accession: B41185 R;Overbergh, L; Torrekens, S; Van Leuven, F; Van den Berghe, H. J. Blol. Chem. 266, 16903-16910, 1991 J. Blol. Chem. 266, 16903-16910, 1991 A;Title: Molecular characterization of the murinoglobulins. A;Reference number: A41185; MUID:91358495; PMID:1840592 A;Accession: B41185 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-1451 <0VE> A;Cross-references: GB:M65238; NID:g199888; PIDN:AAA73041.1; PID:g199889 C;Superfamily: alpha-2-macroglobulin
RESULT 11 S13495 pregnancy zone protein - human C;Species: Homo sapiens (man) R;Devriendt, K; van den Berghe, H; Cassiman, J.J.; Marynen, P. Biochim. Biophys. Acta 1088, 95-103, 1991 A;Title: Primary structure of pregnancy zone protein. Molecular cloning of a full-length A;Reference number: S13495; MUID:91113734; PMID:1989698 A;Reference number: S13495; MUID:91113734; PMID:1989698 A;Residues: not compared with conceptual translation A;Molecular type: mRNA A;Residues: 1-1482 cDEV> A;Cross-references: EMBL:X54380; NID:935824; PIDN:CAA38255.1; PID:935825 A;Cross-references: EMBL:X54380; NID:935824; PIDN:CAA38255.1; DID:935825 A;Cross-references: EMBL:X54380; NID:935824; PIDN:CAA38255.1; DID:935825	Qy 1102 -PKAKEALNMLTWRAEQEGGMQFWVSSESKLSDSWQPRSLDIEVAAYALLSHFL 1154	Db 925 SDAEISEKMSLVLPPTVVKDSARAHFSVMGDILSSAIKNTQNLLHMPYGCGEQNMVL 981 Qy 929 FARNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGST 986	680

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A;Cross-references: GDB:120330; OMIM:176420
A;Cross-references: GDB:120130; OMIM:176420
A;Map position: 12p13-12p12.2
A;Introns: 73/3; 116/2; 146/3; 169/3; 703/1; 7a;Introns: 73/3; 116/2; 146/3; 169/3; 703/1; 7a;Introns: The list of introns may be incomplete C;Superfamily: alpha-2-macroglobulin
E;685-735/Region: bait region
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A;Molecule type: protein
A;Residues: 670-752,'Q',754-759
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J. Biol. Chem. 264, 15781-15789, 1989
A;Title: The alpha-macroglobulin bait region.
A;Reference number: A34230; MUID:89380162; PM.
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A; Residues: 668-690, 'M', 692-753 <MAR>
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A;Title: A genetic polymorphism in a functional domain of human pregnancy zone
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Best Local
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                                                                                                      KAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELE------
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                                                              QSPPASHAHLQVAAA-PQSLCALRAVDQSVLLMKPEAELSVSSVYNLLTVKDLTNFPDNV
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                           -LYNTGYYLGMFMNS---FAVFQECGLWVLTDANLTKDYIDGVYDN
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IVDVKMVSGFIPLKPTVKMLERSSSVSRTEVSNNHVLIXVEQVTNQTLSFSFMVLQDIPV 1445
                                                                                                                                                                                                                     VYNVKASGSSRRRRSIQNQEAFDLDVAVKENKDDLN--HVDLNVCTSFSGPGR---
                                                                                                                                                                                                                                                                  TRTEKT-AQVTVQDSQTFSTNFQVDNNNLLLLQQISLPELPGEYVITVTGERCVYLQTSM
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GDLKPAIVKVYDYYETDESVVAEY 1469
                                   SNTQDASVSIVDYYEPRRQAVRSY 1378
                                                                                                                              LMEVNLLSGFMVPSEAISL---SETVKKVEYDHGKLNLYLDSVNETQFCVNIPAVRNFKV
                                                                                                                                                                             KYNILPE-----KEDSPFALKVQTVPQTCDGHKAHTSFQISLTISYTGNRPASNMV
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A41185
alpha-2 macroglobulin MUG1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change
C;Accession: A41185
C;Accession: A41185
J. Biol. Chem. 266, 16903-16910, 1991
A;Title: Molecular characterization of the murinoglobulins.
A;Reference number: A41185; MUID:91358495; PMID:1840592
A;Accession: A41185
A;Status: preliminary
A;Molecule type: mRNA

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A;Cross-references: GB:M65736
C;Superfamily: alpha-2-macroglobulin
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                           SVQLEASPDFTAVPVGDD-----QDSYCLSANGRHTSSWLVTPKSLGNVNFSVSAEAQQ
                                                        KVIIEKSDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALSPT
                                                                                     RTTLSKRPEEPPRKDPSSNDPLTETIRKYFPETWVWDIVTVNSTGLAEVEMTVPDTITEW
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 -DAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---LAEFSIDTTCISGSS-LHIKVNHKEEDSCSYFYCMEE
                                                                                                                                                                ----VRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSW
:||:|||||
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                                                   A; Molecule type: mRNA
A; Residues: 20-1473 <ANIZ>
A; Cross-references: EMBL:X78801; NID:g671863; PIDN:CAA55385.
A; Cross-references: EMBL:X78801; NID:g671863; PIDN:CAA55385.
A; Cross-references: EMBL:X78801; NID:g671863; PIDN:CAA55385.
A; Nielsen, K.L.; Sottrup-Jensen, L.
Biochim. Biophys. Acta 1162, 230-233, 1993
A; Title: Evidence from sequence analysis that hen egg-white
A; Reference number: S29836; MUID:93192299; PMID:7680577
                                                                                                                                                                                                                                DNA Seq. 5, 111-119, 1994
A,Title: Amino acid sequence of hen ovomacroglobulin (ovostatin)
A,Reference number: I50671; MUID:95218210; PMID:7535598
A,Accession: I50671
A,Accession: Translated from GB/EMBL/DDBJ
                                                                                                                                                                         A; Accession: I50672
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A; Residues: 1-1473 <NIE>
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N;Alternate names: ovomacroglobulin
C;Species: Gallus gallus (chicken)
C;Species: O5-Jun-1987 #sequence revision 13-Mar-1997 #text_change 31-Mar-2000
C;Accession: I50671; I50672; S29836; A20872; A33715
R;Nielsen, K.L.; Sottrup-Jensen, L.; Nagase, H.; Thogersen, H.C.; Etzerodt, DNA Seq. 5, 111-119, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPNIDVQESIHFLES----EFSRGISDNYTLALITYALSSVGSP-KAKEALNMLTWRAE
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ovostatin precursor - chicken

deduced 3

from

cloned

CDN

A; Cross-references: EMBL: X78801; NID: g671863; PIDN: CAA55384.1; PID:g671864

A;Status: translated from GB/EMBL/DDBJ

PID:g671865

ovomacroglobulin

(ovostatin)

A;Molecule type: protein
A;Residues: 977-980,'N',981-1007,'M',1009,'K',1010-1028 <NI3>R;Nagase, H.; Harris Jr., E.D.; Woessner Jr., J.F.; Brew, K.

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J. Biol. Chem. 258, 7481-7489, 1983
A;Title: Ovostatin: a novel proteinase inhibitor from chicken egg white. I. Purification A;Reference number: A92427; MUID:83238315; PMID:6408074
A;Accession: A20872
A;Molecule type: protein
A;Residues: 37-49 <NAGS
R;Enghild, J. J.; Salvesen, G.; Brew, K.; Nagase, H.
J. Biol. Chem. 264, 8779-8785, 1989
A;Title: Interaction of human rheumatoid synovial collagenase (matrix metalloproteinase kinetics and identification of matrix metalloproteinase cleavage sites.
A;Reference number: A33715; MUID:89255343; PMID:2470748
A;Accession: A33715
A;Molecule type: protein
A;Residues: 710-717, '1', 719, 'T', 721, 'A', 723-742, 'L' <ENG>
C;Superfamily: alpha-2-macroglobulin
C;Keywords: alternative initiators; egg white; proteinase inhibitor
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                           SKIRQPTVCTRETVRPPSYFLNAGFTASTHHVKLSAEVARE--ERGKRHILET-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YCSMNSKHLNGTITAKYTYGKPVKGDVTLTFL-PLSFWGKKK-----NITKTFKINGSA
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27.0%;
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                                                                  ---DGVYDNAEYAERFMEENEGHIVDIHDFSLGS
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A;Molecule type: mRNA
A;Residues: 1-1500 <MRR>
A;Residues: 1-1500 <MRR>
A;Cross-references: GB:M84000; GB:J05359; NID:g205383; PI
A;Cross-references: GB:M84000; GB:J05359; NID:g205383; PI
A;Experimental source: strain Sprague-Dawley, liver
A;Note: sequence extracted from NCBI backbone (NCBIP:8716
R;Ionberg-Holm, K.; Reed, D.L.; Roberts, R.C.; Hebert, R.
J. Biol. Chem. 262, 438-445, 1987
A;Title: Three high molecular weight protease inhibitors
A;Reference number: A26124; MUID:87083487; PMID:2432067
                                                                                                                                                                                                                                                                   C;Accession: A42210; A26124
R;Warmegard, B.; Martin, N.; Johansson,
Biochemistry 31, 2346-2352, 1992
                                                                                                                                                                                                                                                                                                                          A42210
alpha-1-macroglobulin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
                                                                                                                                                                                                                       A;Title: cDNA cloning and sequencing of rat alpha 1-macroglobulin A;Reference number: A42210; MUID:92172859; PMID:1371696
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                                                                    Hebert, R.R.;
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                           plasma.
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                                                                    M.C.;
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A;Accession: A26124
A;Molecule type: protein
A;Residues: 25-29, 'F',31-44 <LON>
A;Residues: 25-29, 'F',31-44 <LON>
C;Superfamily: alpha-2-macroglobulin
C;Keywords: glycoprotein; plasma; proteinase inhibitor
C;Keywords: glycoprotein; plasma; proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-1474/Product: alpha-1-macroglobin #status predict;
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TSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTA---LSP--
                                                                                                EVAQEVEVRETVRKYFPETWIWDMVPLDLSGDGELPVKVPDTITEWKASAFCLSGTTGLG
                                                                                                                                                                                                                              LPQKAEQGAYLGPLPYKGGENCIKAEDITHNGIVYTPKQDLNDNDAYSVFQSIGLKIFTN
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                              LSST-ISHKVFQPFFLELTLPYSVVRGEAFILKATVLNYMPHCIRIHVSLEMSPDFLAVP
                                                               LTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILM
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murinoglobulin precursor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Jan-1997 #sequence_revision
                                R; Iwasaki, H.; Suzuki, Y.; Sinohara, J. Biochem. 120, 1167-1175, 1996
                                                                   C; Accession: JC5144
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A;Molecule type: mRNA A;Residues: 1-1464 <IWA> A;Cross-references: DDBJ:D84339 C;Superfamily: alpha-2-macroglobulin F;1-23/Domain: signal sequence #status Ş 밁 S A;Status: preliminary A; Accession: JC5144 A; Reference number: JC5143; A; Contents: liver A;Title: Cloning and sequencing of cDNAs er A;Reference number: JC5143; MUID:97164019; Query Match Local Similarity 16 73 13 VLEA-LALLMTAASVHKKPQYMVLVP-LCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVS 18.7%; ilarity 27.9%; Conservative 24 243; -EGVFEKGSFKTLTLPSLPLNSADETYELRVTGRTQDETLFSNS Score 1374.5; Pred. No. 1.1e. 43; Mismatches predicted <SIG> -TQLYTEVPEKSCLHLHYLKETVTVSAS DB 2; 596; Indels Length 1464; 271; Gaps 63 72 murinog

1085 1134	1033 VIHSELQGGNKSPVTLTAXIVTSLLGYRKYQPNIDVQESIHFLESEFSRGISD : :: :	
1032 1076	975 SAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDPGR	
974 1016	915 IRMPYGCGEONMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSF 	
914 956	855 GIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQITAIGDVLGPSINGLASL 	
854 899	812 SEDG-ATVLFPIRPTHLGEIPITVTALSPTASDAVTQMILVKAE	
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751 786	692 ETWIWLDTNMGYRIYQEFEVTVÞDSITSWVATGFVISEDLGLGLTTTTPVELQAFQPFFIF	
691 727	640 VLTDANLTKDYIDGVYDNAEYAERFMEENEGHIVDIHDFSLGSSPHVRKHFF	
639 677	606 TMENVVHELELYNTGYYLGMFMNSFAVFQECGLW : :: : : : : : : : :	
605 617	YWSKVKAEPSE : ; ; ; SFRPAQSLPAS	
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335 345	296DEBMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGIS : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :	
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237 237	179 WLSQQSDLGVISKTFQLSSHPILGDWSIQV-QVNDQTYYQSFQVSEYVLPKFEVTLQTPL	
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1357 EVSYTGRRÞASNMAIVNVKMISGFSÞLKSTVKMLERSDHVSRTEVNKNNVLIYVDQVTNE 1416	Db 13!
1287 SFSGPGRSGMALMEVNILLSGFMVPSEAISLSETVKKVEYDHGKLNLYLDSVNET 1340	Оу 121
1306 SVSGEGCVYTQTALKYNVFLEKEKYAFALQVHTVPQTCDDPKAHKRFQISL 1356	Db 13
1229 SANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDV-AVKENKDDLN-HVDLNVCT 1286	Оу 12:
1251 ALSRYGAATFGRTGKTALVKIQSSGTFSTKFQVDNSNRLLLQQVSLPHIPEEYTI 1305	Db 12!
1190 ALSEFAALPMAVNI 1228	Оу 11:
1195 AEVEMTSYVLLAHLTAQGTPTPEEMTSAMRIVNWITKQQNSYGGFSSTQDTVVALH 1250	11:
1140 LDIEVAAYALLSHFLQEQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALK 1189	ογ 11,
1135 VYTKALLAYAFALAGNQDKRKEILKSLDEEAVKEDNSIHWERPQKPRRPEALLYQPQAPS 1194	рь 11:
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Search completed: January 15, 2004, 18:14:44 Job time : 39 secs

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RESULT 2
A2MG HUMAN STANDARD; PRT; 1474 AA.
ID 7A2MG HUMAN STANDARD; PRT; 1474 AA.
AC P01023; 013677;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Alpha-2-macroglobulin precursor (Alpha-2-M).
GN A2M.
OS Homo sapiens (Human).
OC Mammalia; Eutheria; Primates; Catarrhini; Homini
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       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Hall P.K., Nelles L.P., Travis J., Roi
"Proteolytic cleavage sites on alpha
"hading are different for
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Magnusson S.;
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Jones C.M., Loenbl
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                                                    aureus V-8 proteinase.",
Biochem. Biophys. Res. (
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Kan C.-C., Solomon E., Belt K.T.,
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Loenblad P.B., Magnusson
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         Sottrup-Jensen
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          PubMed=6172288;
ottrup-Jensen L.,
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ad P.B., Magnusson S., Petersen T.E.;
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184:596-603(1992).
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for trypsin and
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EMBL; Z11711; CAA77774.1; --
EMBL; M36501; AAA51552.1; --
EMBL; X68728; CAA48670.1; --
EMBL; X68729; CAA48670.1; JO:
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Genet. 88:313-319(1992).

-i- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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"Cloning of the human alpha
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Poller W., Faber J.-P., Olek K.;
"Sequence polymorphism in the human alpha2-macroglobulin
Nucleic Acids Res. 19:198-198(1991).
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                                            3D-structure;
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MEDLINE=92128897; PubMed=1370808;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A COMPORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH TRAPS THE BROTEINASE. THE ENTRAPED ENZYME REMAINS ACTIVE AGAINST LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES (ENTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE BAIT REGION A THIOLESTER BOND IS YENDROLYZED AND MEDIATES THE COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.

SUBUNIT: HOMOTETRAMER, WHICH CONSISTS OF TWO PAIRS OF DISULFIDELINKED CHAINS.

TISSUE SPECIFICITY: Plasma.

MISCELLANEOUS: CONTRARY TO THE RAT PROTEIN, WHICH IS AN ACUTE PHASE PROTEIN, THIS PROTEIN IS ALWAYS PRESENT AT HIGH LEVELS IN CITECULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIRCULATION.
SIMILARITY: TO OTHER PROTEINS OF INCLUDING COMPLEMENT COMPONENTS
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                                                                                                                                                                    103950;
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                                                            protease inhibitor;
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                                                                                                                      IPR001599; MacrogloblnA2
                                                                                                                                                                                                                                                                                                                                 equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                               30-SEP-98.
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                                            Polymorphism;
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numan alpha 2-macroglobulin gene and
functional domains: the bait region
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                                            ALPHA 2 MACROGLOBULIN; 1. nhibitor; Glycoprotein; Plasma; ymorphism; Thioester bond.
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ic residues required for receptor binding to t
f the receptor binding domain of human alpha2-
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ALPHA-2-MACROGLOBULIN
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        VK--TKVFQLKR-----KEYEMK------LHTEAQIQEEGTVVELTGRQSSEITRTI
                                          KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT----TVTESV
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266; Mismatches 551; Indels 284;
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                                                                                                     QKPKAPVGHFYEPQAPSAEVEMTSYVLLA-YLTAQPAPTSEDLTSATNIVKWITKQQNAQ
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                                                                           GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS
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                             LPELPGEYSMKVTGEGCVYLQTSLKYNI-----
                                                        ----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK----ENKD
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            use by non-prefit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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Kunz D., Zimmermann R., Heisig M., Heinrich P.C.;
"Identification of the promoter sequences involved in the interleukin-6 dependent expression of the rat alpha 2-macroglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of its messenger RNA.";
J. Biol. Chem. 262:446:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gehring M.R., Shiels B.R., Northemann W., de Kan C.-C., Chain A.C., Noonan D.J., Fey G.H.; Sequence of rat liver alpha 2-macroglobulin
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01-JAN-1988 (Rel. 06, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-2-macroglobulin precursor (Alpha-2-M).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87083488; PubMed=2432068;
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                                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no rest
                                                                                                                                                                                        LINKED CHAINS.
TISSUE SPECIFICITY: Plasma.
INDUCTION: BY INFLAMMATORY STIMULUS THE LEVEL
INDUCTION: BY INFLAMMATORY STIMULUS THE LEVEL
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FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH, CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES FOR DIFFERENT PROFEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH TRAPS THE PROTEINASE. THE ENTRAPED ENZYME REMAINS ACTIVE AGAINST LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES (BOND IS YDROLVZED AND MEDIATES THE BAIT REGION A THIOLESTER BOND IS SYDROLVZED AND MEDIATES THE COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.

SUBUNIT: HOMOTETRAMER, WHICH CONSISTS OF TWO PAIRS OF DISULFIDE-TIME TO THE PROTEINASE.
                                                                                                                                            FIRST INCREASES, THEN DECREASES AFTER A MAXIMUM. SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACRO INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
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Eutheria; Rodentia;
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EMBL; X13984; CAA322164.1; JOINED.
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EMBL; M11792; AAA40637.1; -.
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Pfam; PF01835; A2M_N;
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DYTVKVTGEGCVYLQTSLKYSV----
                                                                                                                                                                                              LWYQPQATSAEVEMTAYVLLAYL----TTEPAPTQEDLTAAMLIVKWLTKQQNSHGGFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYFPETWIWDLVVVDSAGVAEVEVTVPDTITEWKAGAFCLSNDTGLGLSPV-VQFQAFQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLKEL--SYMVVSRGQLVAVG-----KQNSTM--FS--LTPENSWTPKACVIVYYIEDD
                                                                                                                                                                                                                                                                                                RGGAGGSHVYTKALLAYAFALAGNQDTKKEILKSLDEEAVKEEDSVHWTRPQ-KPSVSVG
                                                                                                                                                                                                                                                                                                                                                                                                                                             SNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YQREDGSFSAFGNYDPSG----STWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLKGHQK 1022
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                                           AVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK----ENKDDLNHV
                                                                                            TQDTVVALHALSKYGSATFTRAKKAAQVTIRSSGTFSTKFQVNNNNQLLLQRVTLPTVPG
                                                                                                                                             TODTTVALKALSER- AALMNTERTNIQVTVTGPSSPSPLAVVQ-----
                                                                                                                                                                                                                                               --WQPR--SLDIEVAAYALLSHFLQFQTSEGIP----
                                                                                                                                                                                                                                                                                                                                              --SRGISDNYTLALITYALSSVGSPKA-KEALNMLTWRAEQEGGMQFWVSSESKLSDS--
                                                                                                                                                                                                                                                                                                                                                                                               DNGCFRSSGSLLNNAMKGGVEDEVTLSAYITIALLEMSLPVTHPVVRNALFCLDTAWKSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - CICMNORHTASWAVIPKSLGNVNFTVSAEALNSKELCGNEVPVVPEOGKKDTIIKSLLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - FAVFQECGLWVLTDANLTKDYI - DGVYDNAEYAERFMEENEGHIVDIHDFSLGSSPHVR
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·LPREEEFPFAVVVQTLPGTCEDPKAHT
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"Molecular characterization of the murinoglobulins.";

J. Biol. Chem. 266:16903-16910 (1991).

-i- FUNCTION: A PROTEINASE ACTIVATES THE INHIBITOR BY SPECIFIC PROTEOLYSIS IN THE BAIT REGION, WHICH, BY AN UNKNOWN MECHANISM LEADS TO REACTION AT THE CYSTEINYL-GLUTAMYL INTERNAL THIOL ESTER SITE AND TO A CONFORMATIONAL CHANGE, WHEREBY THE PROTEINASE IS TRAPPED AND/OR COVALENTLY BOUND TO THE INHIBITOR. WHILE IN THE TETHRAMERIC PROTEINASE INHIBITORS STERIC INHIBITION IS SUFFICIENTLY STRONG, MONOMERIC FORMS NEED A COVALENT LINKAGE BETWEEN THE ACTIVATED GLUTAMYL RESIDUE OF THE ORIGINAL THIOL ESTER AND A TERMINAL AMINO GROUP OF A LYSINE OR ANOTHER NUCLEOPHILIC GROUP ON THE PROTEINASE, FOR INHIBITION TO BE EFFECTIVE.
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P28665;
01-DEC-1992
                                                                                                                                                                                                                                                                                            Pfam; PF00207; A2M; 1.
Pfam; PF0183; A2M N; 1.
PROSITE; PS00477; ALPHA 2 MACROGLOBULIN;
Serine protease inhibitor; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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01-NOV-1995 (Rel. 32, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Murinoglobulin 1 precursor (MuG1).
MUG1 OR MUG-1.
                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                   Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Mammalia; Eutheria;
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MGD; MGI:99837; Mug1.
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                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002890; A2M_N.
InterPro; IPR001599; MacrogloblnA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: MONOMER:
TISSUE SPECIFICITY: Plasma.
SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACRO
INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
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Rodentia;
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MURINOGLOBULIN 1
BAIT REGION (APP
BY SIMILARITY.
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Sciurognathi;
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thi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                               1.
Plasma;
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DE Murinoglobulin 2 precursor (MuG2
GN MUG2 OR MUG-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cr.
OC Mammalia; Eutheria; Rodentia; Sc
NCBI TaxID=10090;
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                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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MGD; MG1:9983; Mug2.
InterPro; IPR002599; MacrogloblnA2.
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Serine protease inhibitor; Glycoprotein; Plasma;
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Pfam; PF01835; A2M_N; 1.
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SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
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een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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                                                  FAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFG--NYDPSGST
                                                                                                                                KSLGNVNFSVSVEAQQSSEPCGSEVATVPATGRKDTVVKVLIVEPEGIKQEHTFNSLFCA
                                                                                                                                                                                                                              SNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEYA
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                                   FAPNIYYLKYLDKTQQLTQKIKTKALGFLRAGYQRELNYKHKDGSYSAFGDQNGEREGNT
                                                                                  SDAEIS---EKMSLVLPPTVVKDSARAHFSVMGDILSSAIKNTQNLLHMPYGCGEQNMVL
                                                                                                         TUNRLOSTLKTLSFSFPPNTVTGSERVQITAIGDVLGPSINGLASLIRMPYGCGEQNMIN
                                                                                                                                                         THLGEIPITVTALSPTAS-----
                                                                                                                                                                               MNYLPTSMRMSVQLEASPDFTAVPVGDDHDSYCLSANGRHTSSWLV------TP
                                                                                                                                                                                                    FNYLKDATEVKVIIEKSDKFDILMTSSE-----INATG-HQQTLLVPSEDGATVLFPIRP
                                                                                                                                                                                                                                                                             SSEVSGTLQKGSSKRPQPEEPPREDPPRKDPLAETIRKYFPETWVWDIVTVNSTGVAEVE
                                                                                                                                                                                                                                                                                                                            EKHTDWVPHGREKDVYRYVED-----MDLKAFTNLKIKLPKICFDSAPMSGPRGKFDLAF
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                                                                                                                                              -DAVTQMILVKAEGIEKSYSQSILLDL
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MEDLINE=91113734; PubMed=1989698;
MEDLINE=91113734; PubMed=1989698;
Devriendt K., van den Berghe H., Cassiman J.-J., Marynen P.;
"Primary structure of pregnancy zone protein. Molecular cloning full-length PZP cDNA clone by the polymerase chain reaction.";
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MEDLINE=86059456; PubMed=2415522;
Sand O., Folkersen J., Westergaard J.G., S
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                                                                                                                                                                  Marynen P., Devriendt K., van den Berghe H., Cassiman J.-J.; "A genetic polymorphism in a functional domain of human pregnancy zone protein: the bait region. Genomic structure of the bait doma of human pregnancy zone protein and alpha 2 macroglobulin."; FEBS Lett. 262:349-352(1990).
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MEDLINE=89380162; PubMed=2476433;
Sottrup-Jensen L., Sand O., Kristensen L., Fey
"The alpha-macroglobulin bait region. Sequence
localization of cleavage sites for proteinases
alpha-macroglobulins.";
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                              MEDLINE=90242963; PubMed=1692292;
                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Placenta;
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                                                                                                     SEQUENCE OF 974-983.
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Biochemistry 28:9324-9331(1989).

-i- FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH, CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH TRAPS THE PROTEINASE. THE ENTRAPPED ENZYME REMAINS ACTIVE AGAINST LOW MOLECULAR WEIGHT SUBSTRATES (ACTIVITY AGAINST HIGH MOLECULAR WEIGHT SUBSTRATES IS GRATLY REDUCED). FOLLOWING CLEAVAGE IN THE BAIT REGION A THIOLESTER BOND IS HYDROLYZED AND MEDIATES THE COVALENT BINDING OF THE PROTEIN TO THE PROTEINASE.

-i- SUBBUNIT: HOMOTETRAMER, WHICH CONSISTS OF TWO PAIRS OF DISULFIDE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Biol. [5]
                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
entities requires a license agreement (See http://www.isb
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                            MIM;
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                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                               Pfam; PF00207; A2M; 1
Pfam; PF01835; A2M N;
                                                                                                                                                                                                                                                        GG; GO:0016975; F:alpha-2 macroglobulin; GO; GO:0007565; P:pregnancy; TAS. InterPro; IPR002890; A2M N. InterPro; IPR001599; MacrogloblnA2.
                                                                                                                                                                                                                                                                                                                                               EMBL; X54380; CAA38255.1; -.
EMBL; M24416; AAA60234.1; -.
EMBL; X51541; CAA35919.1; -.
PIR; S13495; S13495.
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Gene 81:325-334(1989).
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Cassiman J.-J., Marynen
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             1BV8.
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                            TISSUBLEGg white;
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MEDLINE-83238315; PubMed=6408074;
Medline-83238315; PubMed=6408074;
Moessner J.F., Brew K.;
Nagase H., Harris E.D. Jr., Woessner J.F., Brew K.;
"Ovostatin: a novel proteinase inhibitor from chicken egg white. I "Ovostation, physicochemical properties, and tissue distribution Purification, physicochemical properties, and tissue distribution
                                                                                                                                                                                                                                                                                                                                     P20740;

P20740;

01-FEB-1991 (Rel. 17, Created)

01-NOV-1995 (Rel. 32, Last sequence update)

01-NOV-1995 (Rel. 32, Last annotation update)

Ovostatin precursor (Ovomacroglobulin).

Gallus gallus (Chicken).

Gallus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasianinae;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
              J. Biol.
[3]
                                                                                                                                                                                 "Amino acid sequence of hen cloned cDNA.";
                                                                                                                                                                                                                   Etzerodt M.;
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                                                                                                                                        SEQUENCE OF 37-49.
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MEDLINE=93192299; PubMed=7680577;
Nielsen K.L., Sottrup-Jensen L.;
"Evidence from sequence analysis that hen egg-white ovomacroglobulin sequence from sequence analysis that hen egg-white ovomacroglobulin is devoid of an internal beta-Cys-gamma-Glu thiol
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GO; GO:00171114; F:wide-spectrum pro
InterPro; IPR002890; AZM_N.
InterPro; IPR001599; MacrogloblnA2.
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EMBL; X78801; CAA55385.1;
PIR; I50671; A20872.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: CONTAINS 56 MOL GLUCOSAMINE PER MOL SUBUNIT. SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY, INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
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  TRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNIL-IKDPKSNLIQQ
                                                                                                                AALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVS---VL
                               EYDTINTTIFEKNTTTSNGLQCLNFMIPPVTSVSLAFISFTAKGTTFDLKERRSVMIWNM
                                                           EAE----GVFEKGSFKTLTLPSL-----PLNSADEIY-ELRVTGRTQD-----EILFSNS
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                                           ATKQKTDGCFQSTGILVNNAMKGGVENELSLSAYITIALLEAGHSMSHTVIRNAFYCLET
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                                                                     KGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLES
                                                                                                 VSGYOKOLSYKHPDGSYSTFGIRDKEGNTWLTAFVYKSFAEASRFIYIDDNVQAQTLIWL
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A2MG MOUSE S
Q61838; Q60628;
Q1-NOV-1997 (Rel
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Umans L., Serneels L., Hilliker C., Stas L., Overbergh L.,
de Strooper B., van Leuven F., van den Berghe H.;
"Molecular cloning of the mouse gene coding for alpha 2-macroglobulin
and targeting of the gene in embryonic stem cells.";
Genomics 22:519-529(1994).
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Mammalia; Eutheria;
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01-NOV-1997 (Rel. 35,
15-SEP-2003 (Rel. 42,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93076803;
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                                                                                                                                                                                                                          FUNCTION: IS ABLE TO INHIBIT ALL FOUR CLASSES OF PROTEINASES BY A UNIQUE "TRAPPING" MECHANISM. THIS PROTEIN HAS A PEPTIDE STRETCH, CALLED THE 'BAIT REGION' WHICH CONTAINS SPECIFIC CLEAVAGE SITES FOR DIFFERENT PROTEINASES. WHEN A PROTEINASE CLEAVES THE BAIT REGION, A CONFORMATIONAL CHANGE IS INDUCED IN THE PROTEIN WHICH TRAPS THE PROTEINASES. THE ENTEAPPED ENZYME REMAINS ACTIVE AGALNST LOW MOLECULAR WEIGHT SUBSTRATES IS GREATLY REDUCED). FOLLOWING CLEAVAGE IN THE BAIT REGION A THIOLESTER BOND IS FURDROLLYZED AND MEDIATES THE COLLEGE OF THE PROTEIN HER STREET HER BAIT REGION A THIOLESTER BOND IS FURDROLLYZED AND MEDIATES THE COLLEGE OF THE PROTEIN HER STREET HER BAIT REGION A THIOLESTER BOND IS FURDROLLYZED AND MEDIATES THE COLLEGE OF THE PROTEIN HER STREET HER BAIT REGION A THIOLESTER BOND IS FURDROLLYZED AND MEDIATES THE COLLEGE OF THE PROTEIN HER STREET HER BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT THE BAIT REGION AT T
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                                                                            IN CIRCULATION.

STMTLARITY: TO OTHER
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DEVELOPMENTAL STAGE: CONTRARY TO THE RA
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                                                       INCLUDING COMPLEMENT
                                                                                                                                 ACUTE PHASE PROTEIN,
     SWISS-PROT entry
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letazoa; Chordata;
ltheria; Rodentia;
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Last annotation update)
precursor (Alpha-2-M).
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                                                                               ALPHA-MACROGLOBULIN FAMILY,
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  produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Serine protease
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HSSP; P01023; 18V8.
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GO:0016975; F:alpha-2 macroglobulin;
181
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LAGGLHQLSFPLSVEPALGIYKVVVQKDSGKKIEHSFEVKEYVLPKFEVIIKMQKTMAFL
             SDLGVISKTFQLSSHPILGDWSIQVQVND-QTYYQSFQVSEYVLPKFEVTLQTPLYCSMN
                                                      ETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNIL-IKDPKSNLIQQWLSQQ 183
                                                                                                 SNLTVSVLEAEGYFEKGSF--KTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSF
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ALPHA-2-MACROGLOBULIN 165 kDa SUBUNIT
ALPHA-2-MACROGLOBULIN 35 kDa SUBUNIT.
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                                                                                                                                                                                                    SEFSRGISDN----YTLALITYALSSVGS-PKAKEALNMLTWRAEQEGGMQFWVS----
                                                                                                                                                                                                                                                                                                                                                                                        GYQRELLYQREDGSFSAFGNY---DPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHKDTVVKSVIVEPEGIEKEQTYNTLLCPQDTELQD---NSSLELPPNVVEGSARATHSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALSPTA--------
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SLGGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPS--
                                                QKVKALSFYQPRAPSAEVEMTAYVLLAYLTSESSRPTRDLSSSDLSTASKIVKWISKQQN
                                                                                                SESKLSDSWOPR -- SLDIEVAAYALLSHFLQFQT-
                                                                                                                                                    TAWA-SISQSQESHVYTKALLAYAFALAGNKAKRSELLESLNKDAVKEEDSLHWQRPGDV
                                                                                                                                                                                                                                                          LSMKOKENGCFQQSGYLLNNAMKGGVDDEVTLSAYITIALLEMPLPVTHSAVRNALFCLE
                                                                                                                                                                                                                                                                                                        LKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -LAVPVGGHENSHCICGNERKTVSWAVTPKSLGEVNFTRTAEALESQELCGNKLTEVPAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----NASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTK---
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             InterPro; IPRO01134; Netrin_C.

Pfam; PF00207; AZM, 1.

Pfam; PF01035; AZM, 1.

Pfam; PF01035; AZM, 1.

Pfam; PF011759; NUTR; 1.

Pfam; PF01759; NUTR; 1.

ProDom; PD003264; Anaphylatoxin; 1.

SMART; SM00104; ANATO; 1.

SMART; SM00104; ANATO; 1.

SMART; SM00643; C345C; 1.

SMART; SM00643; C345C; 1.

PROSITE; PS01177; ALDPHA 2 MACROGLOBULIN; 1.

PROSITE; PS01178; ANAPHYLATOXIN 1; 1.

PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAMJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete complementary DNA sequence of the third component of complement of lamprey. Implication for the evolution of thioester containing proteins.";
J. Immunol. 148:3290-3295(1992).
-i- FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. AFTER ACTIVATION (C3B), IT CAN BIND COVALENTLY, VIA 1TS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES. CYCLOSTOMATES C3 APPEARS TO REPRESENT THE COMMON ANCESTOR OF MAMMALIAN C3 AND C4, SHOWING SIMILARITIES TO
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CO3 LAMJA STANDARD; PRT; 1673 AA (200685; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complement C3 precursor [Contains: C3A anaphylatoxin] C3.
                                                                                                                                                                                                                                                                             PIR; 150806; 150806.
HSSP; P01024; 1C3D.
                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=94989;
                                                                                                                                                                                                                                                                                                               EMBL; D10087; BAA00983.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petromyzontiformes;
                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOTH PROTEINS.
SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
SIMILARITY: Contains 1 anaphylatoxin-like domain
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                                                                                                                                                                                                  IPR002890; A2M_N.
IPR000020; Anaphylatoxin.
IPR001599; MacrogloblnA2.
IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Petromyzontidae; Lethenteron.
Plasma; Inflammatory response; Glycoprotein;
                                                                                                                                                                                                                                                                                                                 .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anaphylatoxin-like domain.
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MBL outstation -
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                                                                                                                                               VVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEY------
                                                                                                                                                                                         ELCKSQVSL---SLKGRPTLEPKAMLTLDLIGEPDARVGLLAVDQAVYAVNRKHRLTQDR
                                                                                                                                                                                                               ---PSNEQGELVYTAQKYASASYMHIDV-TRIMRLGETLNVFLTAKTTQLNAVTHFTYMV
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                                        PRQLSMLQIRREAEKYTQEFRKCCVDGLKMSPTGQGCEERLKRVTGPKECVDAFLQCCKK
                                                                                                                  VWKAMETFDTGCTAEGGAGRPGVFSDAGLALITSKGL----NTTDRSEIGCPKVPSRK
                                                                                                                                                                                                                                                                                                                                                                                                                  KEVDVVAKVQVGSAT----INPQKMRTDSNGLTSFTVTPPNVNQLTVTVRTDERH----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVTESVTGISRNVS-TNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---FQVSEYVLPKFEVTLQTPLYCSMNSK----HLNG-----TITAKYTYGKPVKGDVTL
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ALPHA CHAIN (BY SIMILARITY).
GAMMA CHAIN (BY SIMILARITY).
C3A ANAPHYLATOXIN (BY SIMILARITY).
ANAPHYLATOXIN-LIKE.
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(By similarity).
W; 4B5FC756B123A506 CRC64;
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COMPLEMENT C3
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                                                                                                                                                                                                                                                                                                DVAVKENKD-----PGRSG-----PGRSG
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                                                                                                                     MTIIEVNMLTGF-IPDKNDLIQLKESVDKYISNYEITDSVLIIYWDKVPSTEDYCFAFKI
                                                                                                                                                                                                                                              KVTMTEADDGESPOGRLGWFDGKRRRRDIGDEGGVEAVYRMNMCTRYKPRKEDLSSESG
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                                                            VRNFKVSNTQDASVSIVDYYEPRRQAVRSYN---SEVKLSS-C--DLCSDVQGCRPCE 1400
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52 PCB-2003 (Rel. 01, Created)
51 Complement C4 precursor [Contains cupdate)
61 CO4 CO4 AND C4B.
62 Homo sapiens (Human).
63 Homo sapiens (Human).
64 Homo sapiens (Human).
65 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
65 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
65 NCBI_TaxID=9606;
66 SEQUENCE FROM N.A. (C4A AND C4B).
67 TISSUES-Liver;
67 MEDIJINE-84156544; PubMed=6546707;

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SEQUENCE OF 1-21 FROM N.A.

MEDLINE-9428044; PubMed-8012361;
Sargent C.A., Anderson M.J., Hsieh
Gomez-Escobar N., Campbell R.D.;

"Characterisation of the novel gene
complement C4A gene in the human ma
hum, Mol. Genet. 3:481-488(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4A gene. DNA SCYC.";
21-hydroxylase gene.";
7 Tmmunol. 146:1057-1066(1991).
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Banta A.,
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Harrison R.A., Thomas M.L., Tack B.F.;
"Sequence determination of the thiolester
component of human complement.";
Proc. Natl. Acad. Sci. U.S.A. 78:7388-7392
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-22 AND 1056-1225 FROM MEDLINE=8515626; PubMed=383531; Belt K.T., Yu C.Y., Carroll M.C., "Polymorphism of human complement
                                                                                                                                                                                                                           human complement component C4. Biochem. J. 199:359-370(1981).
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                  "Identification of the site of su
                                      MEDLINE=86111851;
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, Swartzell S., Se
e determination of
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tural basis of
                                      1405-1431, AND SULFATION 11851; PubMed=3944109;
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PubMed=1988494;
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Smith T.M., Spies
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EMBL; AF019413; AAB67980.1; -.
EMBL; AL049547; CAB89302.1; -.
EMBL; M14823; AAA52292.1; -.
EMBL; M14824; AAA52292.1; -.
EMBL; X77491; CAA54627.1; -.
PIR; I56095; C4HU.

HSSP; P01031; 1KJS. SWISS-2DPAGE; P01028;

GO:0005576; GO:0006958;

C:extracellular;
P:complement acti

activation,

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ANAPHYLATOXIN.

ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT CAPA ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND BASOPHILIC LEUKOCYTES.

-I. SUBUNIT: THIS PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR AND PRIOR TO SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER OF MONIDERICAL CHAINS (ALPHA, BETA, AND GAMMA).

-I. POLYMORPHISM: HUMAN COMPLEMENT COMPONENT C4 IS POLYMORPHIC WITH AT LEAST TWO LOCI, C4A AND C4B. 13 ALLELES OF C4A AND 22 ALLELES OF C4B HAVE BEEN DETECTED. THE ALLELES CARRY THE BLOOD GROUP RODGERS WHILE THE C4B ALLELES CARRY THE BLOOD GROUP RODGERS WHILE THE C4B ALLELES CARRY THE BLOOD GROUP RODGERS WHILE INTERMALED DEFECTS IN C4A ARE the cause of C4A deficiency
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EMBL; K02404; AAA55651.1; -.
EMBL; M59815; AAA51855.1; -.
EMBL; M59816; AAA51855.1; JOINED.
EMBL; U24578; AAA99717.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=87080272; PubMed=2431902; Yu C.Y., Belt K.T., Glies C.M., Campbell R.D., Porter R.R. "Structural basis of the polymorphism of human complement C4A and C4B: gene size, reactivity and antigenicity."; EMBO. J. 5:2873-2881(1986).
                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anderson M.J., Milner C.M., Cotton G.H., Campbell R.D.; "The coding sequence of the hemolytically inactive C4A6 allotype human complement component C4 reveals that a single arginine to typotophan substitution at beta-chain residue 458 is the likely c
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Anderson M.J., Mi
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European Bioinformatics Institute. There a
by non-profit institutions as long as i
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SIMILARITY:
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Pubmed=2431902;
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DE ANTIGENS WHILE C4B ALLOTYPES
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Pfam; PF01821; ANATO; 1.
Pfam; PF01759; NTR; 1.
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GO; GO:0006937; P:regulation of muscle contraction; NAS.
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InterPro; IPR000020; Anaphylatoxin.
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                                                  DYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNS
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PO1029; 061859;
21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Cast annotation update)
SEQUENCE OF
                                                                                                                                                                  SEQUENCE OF 1099-1142 FROM N.A. STRAIN=B10.WR, C57BL/6, C3H/He, CMEDLINE=90353398; PubMed=2387317;
                                                                                                                                                                                                                                                          "Isolation of cDNA clones specifying complement and its isotype, sex-limit Proc. Natl. Acad. Sci. U.S.A. 81:6822
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=85289294; PubMed=2993295;
Nonaka M., Nakayama K., Yeul Y.D., Takahashi M.;
"Complete nucleotide and derived amino acid sequences of component of mouse complement (C4). Evolutionary aspects.
J. Biol. Chem. 260:10936-10943(1985).
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STRAIN=FM; TISSUE=Liver;
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MEDLINE=85298264; PubMed=3862104;
Sepich D.S., Noonan D.J., Ogata R.T.;
"Complete cDNA sequence of the fourth
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                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=85038607;
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Immunol. 139:1568-1577(1987).
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1105-1449
                                                                                                                                                                                                                                                                                                                                      Honjo T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acad.
                                                                                   f N.E.;

yh and C4-low m
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                                             20:1607-1610(1990).
                                                                                                                                                                                                                                                                                                                                                                                      PubMed=6208559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                U.S.A.
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                                                                                             mouse
the is
                                                                                                                                                                                                                                                             pecifying the fourth component of mouse
    sex-limited protein.";
A. 81:6822-6826(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                           isotype-specific
                                                                                                                                                                                        CBA/J,
                                                                                                                 strains have identical
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in mouse
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                                                                                                                                                                                        B10.BR,
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of human
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EMBL; K00019; AAA39554.1;
EMBL; M11729; AAA39506.1;
EMBL; M112968; AAA39558.1;
EMBL; M12970; AAA39556.1;
EMBL; M12970; AAA39556.1;
EMBL; M12979; AAA39559.1;
EMBL; M12969; AAA39557.1;
EMBL; M11789; AAA39557.1;
EMBL; M14789; AAA39561.1;
EMBL; M14425; AAA39561.1;
EMBL; M14425; AAA3964.1;
EMBL; M14226; AAA3964.1;
EMBL; X55495; CAA39112.1;
EMBL; X55495; CAA39114.1;
EMBL; X25495; A24558;
PIR; A24558; A24558.
                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
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and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nonaka M., Nakayama K., Yeul Y.D., Shim: "Molecular cloning and characterization DNA clones for mouse C4 and Slp.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "cDNA clone spanning the alpha-gamma subunit junction precursor of the murine fourth complement component (Proc. Natl. Acad. Sci. U.S.A. 80:5061-5065(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Levi-Strauss M., Tosi M., Steinmetz M., Klein J., Meo "Multiple duplications of complement C4 gene correlate controlled testosterone-independent expression of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=87017050;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-21 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1360-1511 FROM N.A. MEDLINE=83273751; PubMed=6192448; MEDLINE=83273751; Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Proping Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=86031969; PubMed=2997024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of the 5'-flanking regulatory region responsible for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nonaka M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Sequence heterogeneity of murine complementary DNA clones related the C4 and C4-Slp isoforms of the fourth complement component."; Philos. Trans. R. Soc. Lond., B, Biol. Sci. 306:389-394(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tosi M., Levi-Strauss M., Duponchel C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85038859;
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SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. Natl. Acad. Sci. U.S.A. 83:7883-7887(1986)
FUNCTION: C4 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF
CLASSICAL PATHWAY OF THE COMPLEMENT SYSTEM. IT IS PROCE
ACTIVATED C1 WHICH REMOVE FROM THE ALPHA CHAIN THE C4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      difference
Slp genes."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AND, PRIOR TO SECRETION, IS ENZYMATICALLY CLEAV
OF NONIDENTICAL CHAINS (ALPHA, BETA, AND GAMMA)
MISCELLANEOUS: C4 IS A MAJOR HISTOCOMPATIBILITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANAPHYLATOXIN.
SUBUNIT: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kimura H., Yeul Y.D., Yokoyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87:81-99(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO C3, C5 AND ALPHA-2-MACKOGLUBULLIN.
Contains 1 anaphylatoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN IS SYNTHESIZED AS A SINGLE-CHAIN PRECURSOR SECRETION, IS ENZYMATICALLY CLEAVED TO FORM A TRIMER
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                                                                  Sepich D.S.,
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E C4A
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PROSITE; PS01177; ANAPHYLATOXIN 1; 1.
PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
Complement pathway; Plasma; Glycoprotein;
Inflammatory response; Thioester bond.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD003264; Anaphylatoxin; SMART; SM00104; ANATO; 1. SMART; SM00643; C345C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00207; A2M; 1. Pfam; PF01835; A2M N; Pfam; PF01821; ANATO; Pfam; PF01759; NTR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CROSSLNK
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InterPro; IPR00020; Anaphylatoxin.
InterPro; IPR001599; MacrogloblnA2.
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                          179
                                                                                                                       64
                                                                                                                                               63
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                                                                                                                                                                                                                              Similarity
                                                                                   QDEILFSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKD
                                              PKS-NLIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQVQVND---QTYYQSFQVSEYVL
                                                                        ATE---TQGVNLLFSSRRGHIFVQTDQPIYNPGQRVRYRVFALDQKMRPSTDFLTITVEN
                                                                                                                                                                                       AHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAEL------
  PKFEVTLQTP-----LYCSMNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNI-
                                                                                                                      GSCSPKKDFKLSSGDDFVLLSLEVPLEDVRSCGLFDLRRAPHIQLVAQSP--WLRNTAFK
                          SHGLRVLKKEIFTSTSIFQDAFTIPDISEP--GTWKISARFSDGLESNRSTHFEVKKYVL
                                                                                                                                             ------LKTASNLTVSVLEA--EGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRT
                                                                                                                                                                     AWVFSFCASSI----QKPRLLLFSPSVVNLGTPLSVGVQLLDAPPGQ-EVKGSVFLRNPKG
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743
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1416
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224
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570
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14447
1738
753
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24.9%;
                                                                                                                                                                                                                                                                   192870
                                                                                                                                                                                                                    245;
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N-LINKED (GLCNAC...)
F - Y (IN REF. 4).
G -> E (IN REF. 4).
Q -> E (IN REF. 5).
R -> Q (IN REF. 5).
DL -> AI (IN REF. 5).
P -> R (IN REF. 5).
P -> R (IN REF. 5).
D -> E (IN REF. 5).
V -> A (IN REF. 7).
A -> T (IN REF. 7).
K -> N (IN REF. 7).
A -> V (IN REF. 4).
G -> S (IN REF. 4).
G -> S (IN REF. 4).
A -> V (IN REF. 4).
A -> V (IN REF. 4).
A -> V (IN REF. 4).
                                                                                                                                                                                                                  Score 987; DB 1; Length 1738;
Pred. No. 4.8e-46;
From Mismatches 643; Indels 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPLEMENT C4, GAMM
C4A ANAPHYLATOXIN.
ANAPHYLATOXIN-LIKE.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
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(By similarity).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                    D1EE02AE7AB42BFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                C4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sulfation; Signal;
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IEVAAYALLSHFLQFQTSEGIPIM-----RWLSRQRNSLGGFASTQDTTVALKALSEF-A 1195
                                                                                                 IVTSL------LGYRKYQPNIDVQESIHFLESEFSRGISDNYTLALITYALSSVG
                                                                                                                                                                                                                                                                                                                                                                                               VTVPDSITSWVATGFVISEDLGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITI
                                     --KASEDLRNVAHNSLMAMAEETGEHLYWGLVLGSODKVVLRPTAPRSPTEPVPQAPALW
                                                           SPKAKEAL-----NMLTWRAEQEGGMQFW---VSSESK-LSDSWQPRS------LD
                                                                                                                                                                                              YLTKKKQ---LTDNLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLR
                                                                                                                                                                                                                                VPDGDFSSLVRVTASEPLETMGSEGALSP---GGVASLLRLPQGCAEQTMIYLAPTLTASN
                                                                                                                                                                                                                                                                                                    PITVTALSP-TASDAVTQMILVKAEGIEKSYSQSILLDLTD-NRLQSTLKTLSFSFPPN-
                                                                                                                                                                                                                                                                                                                              YNYLND--DVAVSVHVTPVEGLCLAGGGMMA----QQVTVPAGSARPVAFSVVPTAAANV
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                                                                                   VVIALHHGLDVFQDDDAKQLKNRVEASITKANSFLGQKASAGLLGAHAAAITAYALTLT-
                                                                                                                                                      CFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDPGRVIHSELQG---GNKSPVTLTAY
                                                                                                                                                                                YLDRTEOMSKLSPETKDHAVDLIOKGYMRIOQFRKNDGSFGAWLHRD--SSTWLTAFVLK
                                                                                                                                                                                                                                           -----TVTGSERVQITAIGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILD
                                                                                                                                                                                                                                                                              PLKVVARGVFDLGDAVSKILQIEKEG--AIHREELVYNLDPLNNLGRTLE-IPGSSDPNI
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                                                                                                                                                                                                                                                                                                                                                                                                                          SQAHLARNNHNMLQEEDLIDEDDIL-----VRTSFPENWLWRVEPVDSS-----KLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                NEGH-----IVDIHDFSLGSSPHVRKHFPETWIW----LDTNMGYRIYQEFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKLGQYSSPDAKRCCQDGMTKLPMKRTCEQRAARVPQQACREPFLSCCKFAEDLRRNQTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NSYNVGCGPGGGDDALQVFQDAGLAFSDGDRLTQTREDLSCPKEKKSRQKRNVNFQKAVS
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RESULT 12
CO3_ONCMY
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P98093;
01-FEB-1996
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01-FEB-1996 (Rel. 33, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement C3-1 [Contains: C3A anaphylatoxin] (Fragment).
Oncorhynchus mykiss (Raimbow trout) (Salmo gairdneri).
Oncorhynchus mykiss (Raimbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Third component of trout complement. cDNA cloning of functional sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94065166; PubMed=8245455;
Lambris J.D., Lao Z., Pang J., Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8022
            InterPro; IPR002890; A2M N.
InterPro; IPR000200; Anaphylatoxin.
InterPro; IPR001159; MacrogloblnA2.
InterPro; IPR001134; Netrin_C.
                                                                                                 HSSP; P01024; 1C3D
                                                                                                                                                                                                                                                                                                                                                                                                                          Immunol. 151:6123-6134(1993).

FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE CENTRAL ROLE TO THE CENTRAL REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS. AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THOLESTER, TO CELL SURFACE ARBOHYDRATES OR IMMUNE AGGREGATES.

SUBGNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSUE=Liver;
                                                                                                                                                                                                                                                                                                                                                     SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                               RELEASING C3A ANAPHYLATOXIN & GENERATING C3B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1433
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                                                                                                                    ; L24433; AAB05029.1; ALT_INIT.
151339; 151339.
PF00207; A2M;
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                                                                                                                                                                                                                                                                                                                                                 Contains 1 anaphylatoxin-like
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Complement pathway; Complement alternate pathway; Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD003264; Anaphylatoxin; SMART; SM00104; ANATO; 1. SMART; SM00643; C345C; 1.
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Pfam; PF01821; ANATO;
Pfam; PF01759; NTR; 1.
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                 KDGKGVACLKKEHITQTFPKIHDLVKQSI----
                                                                                                                                      TLQTP---LYCSMNSKHLNGTITAKYTYGKPVKGDVTLTF
                                                                                                                                                                               TIFREI-VNPDKGVKSGQFKLPDIVSFGTWHVVTRFQSTPQKTFSSEFEVKEYVLPSFEV
                                                                                                                                                                                                                   LIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQVQVN---DQTYYQSFQVSEYVLPKFEV
                                                                                                                                                                                                                                                            I--FIQTOKTIYTPASTVHYRVFSMTPGLEPLTREIFEDQEVAKNKEIAVSVEIMTPENI
                                                                                                                                                                                                                                                                                                        ISVFIQTDKALYKPKQEVKFRIVTLFSDFKPY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVSVLEAE
                                                   -----KKKNITKTF-KINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT
                                                                                               SL-TPAKAFFYVDDNDLTVDITARYLYGKEVTGTGYVVFGVITTESEKKSFPASLQRVEI
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Pred. No. 6.1e-46;
8; Mismatches 571;
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INTERCHAIN (BY SIMILARITY).
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BETA CHAIN.
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FRAGMENT (BY SIMILARITY).
G FRAGMENT (BY SIMILARITY).
               -FVSVSVLTEGGGEMVEAEKRG-IQIVT
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(BY SIMILARITY)
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                                                         EVAGRAS-----VTKWSIN-NKNQFHTRTDKVNSIDKDLTVKASGNGEATLSVVTLYYA
                                                                                                            TVTGPSSPSPLAVVQPMAVNISANGFGFAICQLNVV---YNVKASGSSRRRRSI-----
                                                                                                                                                                                                                                                                                                                                                 YALSSVGSPKAKEALNMLTWRAEQ----EGGMQFWVSSESKLSDSWQPRSLDIEVAAYALL
                                                                                                                                                                                                                                                                                                                                                                                                             MTAFVLIAMQEASSVCEQSVNSLPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATHYLDNTKKWEDIGLDKRNTAIKYINIGYQRQLAYRKEDGSYAAW--VSRQSSTWLTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILDYLTKKKQLTD---NLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAF 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VPRNQVPNSDADTLISVTA-GEQTSVLVEQAISGDSLGSLIVQPVGCGEQNMIYMTLPVI 100:
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                                                                                                                                                                                                                               SHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNTER----TNIQV
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-----QNQEAFDLDVAVKENKDDLNHVD------LNVCTSFSGPGRSG-MALMEVNLLS
                                                                                                                                                                                                                                                                                           YALANAGKLNKETLLKFASPQLDHWPVPGGYQY------
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PRINTS;

PF01759;

ProDom; PD003264; Anaphylatoxin; 1.

ANAPHYLATOXN

Pfam;

PF01835;

A2M; 1. A2M N; 1. ANATO; 1. NTR;

Netrin_C. Anaphylatoxn. MacrogloblnA2 Anaphylatoxin.

PF01821;

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                                                                                                     InterPro; IPR002890; A InterPro; IPR000220; A InterPro; IPR001840; A InterPro; IPR001599; M InterPro; IPR001134; N
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Q01833;
Q1-JUL-1993
Q1-JUL-1993
15-SEP-2003
                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Elapidae; Elapinae; Naja.
                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93056528; PubMed=1431125; Fritzinger D.C., Connelly M., Petrella E.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Naja naja (Indian cobra).
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                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunol.
                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: C3 precursor is first processed by the removal of 4 Arg residues, forming two chains, beta and alpha, linked by a disulfide bond. C3 convertase activates C3 by cleaving the alpha chain, releasing C3A anaphylatoxin and generating C3B (beta chain + alpha' chain) (By similarity).

SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
SIMILARITY: Contains 1 anaphylatoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTR. COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTR. REACTIVATION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS. AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES. FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3 C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAWMATORY PROCESS. INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR DERMEABILLTY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
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(Rel. 26, Last sequence update)
(Rel. 42, Last annotation update)
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SMART; SM00643; C345C; 1.
SMOSITE; SS00477; ALPHA, 2 MACROGLOBULIN;
PROSITE; PS01177; ANAPHYLATOXIN 1; 1.
PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
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                                                                     RQAIKSMTATAYQTQGGSENYLHVAITSTEIKPGDNLPVNFNVRGNANSLNQIKYFTYLI
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ALPHA CHAIN.
CJA ANAPHYLATOXIN.
CJB (ALPHA CHAIN).
CLEAVAGE (BY C3 CONVERTASE).
ANAPHYLATOXIN-LIKE.
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2.5e-45;
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  KKIDLQLRIQKACAQNVDYVYKTKLLRIEEKDGNDIYFMDV 1553
                                                                                          KHFEVGFIQPGSVKVYSYYNLDEQCTKFYHPDKETGLLNKICHGNICRCAEETCSLLNQQ
                                                                                                                                          RNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHH
                                                                                                                                                                                       ISMLTGFFFDAEDLKRLSNGVDRYISKFEIDNNMAQKGTVVIYLDKVSHSEDECLHFKIH
                                                                                                                                                                                                                                VNLLSGFMVPSEAI-----SLSETVKKVEYDH-----GKLNLYLDSVNETQ-FCVNIPAV
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                                               -----YFMEL
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921 939 869

978 999

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PIR; S15764; C3RT.

PDB; 1QQF; 31-JUL-00.

PDB; 1QSJ; 31-JUL-00.

InterPro; IPR002890; A2M N.

InterPro; IPR0002020; Anaphylatoxin.

InterPro; IPR001599; MacrogloblnA2.

InterPro; IPR001134; Netrin C.
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P01026;
21-JUL-1986
01-AUG-1990
15-SEP-2003
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or send a
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the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Estrogen regulation of tissue-specific expression of complement C3.";
J. Biol. Chem. 264:16941-16947 (1989).

-I. FUNCTION: C3 PLAYS A CENTRAL ROLE IN THE ACTIVATION OF THE
COMPLEMENT SYSTEM. ITS PROCESSING BY C3 CONVERTASE IS THE CENTRAL
REACTION IN BOTH CLASSICAL AND ALTERNATIVE COMPLEMENT PATHWAYS.
AFTER ACTIVATION C3B CAN BIND COVALENTLY, VIA ITS REACTIVE
THIOLESTER, TO CELL SURFACE CARBOHYDRATES OR IMMUNE AGGREGATES.
-I. FUNCTION: DERIVED FROM PROTEOLYTIC DEGRADATION OF COMPLEMENT C3,
C3A ANAPHYLATOXIN IS A MEDIATOR OF LOCAL INFLAMMATORY PROCESS. IT
INDUCES THE CONTRACTION OF SMOOTH MUSCLE, INCREASES VASCULAR
PERMEABILITY AND CAUSES HISTAMINE RELEASE FROM MAST CELLS AND
BASOPHILIC LEUKOCYTES.
-I. SUBUNIT: C3 PRECURSOR IS FIRST PROCESSED BY THE REMOVAL OF 4 ARG
RESIDUES, FORMING TWO CHAINS, BETA & ALPHA, LINKED BY A DISULFIDE
BOND. C3 CONVERTASE ACTIVATES C3 BY CLEAVING THE ALPHA CHAIN,
RELEASING C3A ANAPHYLATOXIN & GENERATING C3B (BETA CHAIN + ALPHA')
                                                                                                                                                                                                                                                                                                                                              use
                                                                                                                                                                                           EMBL; X52477; CAA36716.1;
EMBL; M29866; AAA40837.1;
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J. Biol. C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Purification, characterization, and anaphylatoxin (C3a).";
Biochemistry 17:5031-5038(1978).
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Jacobs J.W., Rubin J.S., Hugli T.E., Bo
Daniels J.S., Daughaday W.H., Bradshaw
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                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
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SMART; SM00104; ANATO; 1.
SMART; SM00643; C345C; 1.
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PROSITE; PS01177; ANAPHYLATOXIN
PROSITE; PS01178; ANAPHYLATOXIN
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PF01821; ANATO;
PF01759; NTR; 1.
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                                                                                                                   ILHSGSDMVEAERSGIPIVTSPYQIHFTKTPKFFKPAMPFDLMVFVTNPDGS
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18; Pred. No. 6.4e-45;
284; Mismatches 609;
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BY SIMILARITY.

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BETA CHAIN.
ALPHA CHAIN.
C3A ANAPHYLATOXIN.
C3B (ALPHA CHAIN)
                                                                                                                                                                              -HDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERR
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nal; 3D-structure;
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                                              LMEVNLLSGFMVPSEAISLSET-----VKKVEYDHGKLN-----LYLDSVNET-QFCVNI
                                                                                                                                                      NVKASGSSRRRRSIQNQEAFDLDVAV-----
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                                                                                                                                                                                                                                                                                                                NVEATSYALLALLLLKDFDSVPPVVRWLNDERYYGGGYGSTQATFMVFQALAQYRADVPD
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                                                                                                                                                                                                                                                                                                                                                                                sequences of cloned cDNA.
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Mammalia;
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"Amino acid sequences of mouse
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A., Wetsel R.A.,
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Sciurognathi; Muridae;
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PROSITE; PS01177; ANAPHYLATOXIN 1; 1.
PROSITE; PS01178; ANAPHYLATOXIN 2; 1.
Complement pathway; Complement alternate path
Inflammatory response; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an
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EMBL; J00369; AAA37336.1; JOINED.
EMBL; J00367; AAA37336.1; JOINED.
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Pfam; PF01835; A2M N; 1.
Pfam; PF01821; ANATO; 1.
Pfam; PF01759; NTR; 1.
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InterPro; IPR000020; Anaphylatoxin.
InterPro; IPR001599; MacrogloblnA2.
InterPro; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                send an email to license@isb-sib.ch).
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MISCELLANBOUS: IC3B IS THE SLOWLY CLEAVED (POSSIBING TO FORM C3C AND C3DG. OTHER PROTEASES PRODUCE OTHER AS C3D OR C3G.

SIMILARITY: TO C4, C5 AND ALPHA-2-MACROGLOBULIN.
SIMILARITY: Contains 1 anaphylatoxin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alternative initiation; MISCELLANEOUS: C3B IS RAP AND A COFACTOR TO FORM IC
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Event=Alternative initiation;
Comment=2 isoforms, Long (shown
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SUBUNIT: C3 precursor is first processed by the removal residues, forming two chains, beta and alpha, linked by disulfide bond. C3 convertase activates C3 by cleaving chain, releasing C3A anaphylatoxin and generating C3B + alpha' chain).
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                                                                                                                                                                                                                                                                                                                                                                                              ; PD003264; Anaphylatoxin; SM00104; ANATO; 1. SM00643; C345C; 1.
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36; Mismatches
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Search completed: January 15, 2004, 18:12:59 Job time: 31 secs

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1: sp archea:*
2: sp bacteria
3: sp fungi:*
4: sp human:*
5: sp inverteb:
6: sp mammal:*
7: sp mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	8	7	6	ហ	4.	ω	N	_	Result No.
1463.5	1491	1542.5	1542.5	1638	1688.5	1692	1693	1699.5	1703	1779.5	1850	3360	4305.5	5360	7326.5	Score
19.9	20.3	21.0	21.0	22.3	23.0	23.0	23.0	23.1	23.2	24.2	25.2	45.7	58.6	72.9	99.7	Query Match
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ALIGNMENTS

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61 ELLKTASNLTVSVLEAEGVPEKGSPKTLTLDSSLPLNSADEIYELRVTGRTQDEILFSNST 120	1 MQGPPILITAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA 60	1 MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA 60	Query Match 99.7%; Score 7326.5; DB 4; Length 1445; Best Local Similarity 98.8%; Pred. No. 0; Matches 1427; Conservative 1; Mismatches 0; Indels 17; Gaps 1;		SEQUENCE 1445 AA; 161719 MW; 6EE6D2D936AF310D CRC64;	WACESON OBJET TALL	PF00207; A2M;	IPR001599;		EMBL; AF410459; AAL84159.1;	02).	macrond-bhilin/Ca CA CE family of thiogeter-containing mortains ".	יים אפשלה אין אין אין אין אין אין אין אין אין אין	LIT M., SUCHELIAND D.K., HOISIAIL W., TOUTY N., YEO E., NAYAR K.,	=21849742; PubMed=11861284;		[1]		Primates; Catarrhini; Hominidae;	Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Enteleostomi:	Homo sariers (Himar)	CD109	-2002 (IIEMBUIEL.	(TrEMBLrel. 21, Last	(TrEMBLrel.	••	Q8TDJ3 PRELIMINARY; PRT; 1445 AA.	ЛТ 1 ,

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              DIEVAAYALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNT
                                                 GDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQG
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                                                                                                       QKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEFS
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DIEVAAYALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNT
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"clated protein.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ day
RMBL; AY083458; AAM00021.1; -.
R InterPro; IPR0012890; A2M N.
R InterPro; IPR001599; MacroglobinA2.
R Pfam; PF00207; A2M; 1.
R Pfam; PF001835; A2M; 1.
R Pfam; PF01835; A2M; N; 1.
R Pfam; PF01835; A2M, N; 1.
R Pfam; PF01835; A2M, N; 1.
R ROSITE; PS00477; ALPHA 2 MACROGLOBULIN; 1.
R ROSUENCE 1442 AA; 161658 MW; E2B9671B8EA5BA
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Matches 1038
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01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
GPI-anchored alpha-2 macroglobulin-related protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                          Hashimoto M., Ichihara M., Takahashi M.; "Cloning and characterization of GPI-anchored related protein.";
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  NVM---
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                                                                         SQKGDLGVVSKTFQLSSNPIFGDWSI
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  -DSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFF
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E2B9671B8EA5BAA7
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NTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHHSSVIFI
                                                                                                                                                                                                                                       AICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVKENKDDLNHVDLNVCTSFSGPGRSG
                                                                                                                                                                                                                                                                                                                                                   EFAALMNTERTNIQVTVTGPSSP------SPLAVVQPMAVNISANGFGF
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Blum H., Bauersa
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Q8N915;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein FLJ38569.
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Homo sapiens (Human).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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 SQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCS
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                ASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDN
                                                                      EIISDYLKI PYQLYFKNKIKLYWSKYKAEPSEKYSLRI SYTQPDSIYGIYAYDKSYNLMN
                                                                                                                                    SPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVI VYYI EDDG
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ASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDN
                                                                                                                 SPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYYIEDDG
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Query Match
Best Local (
  Matches
                                                     Wormbep; ZK337.1a; CE16718.

Wormbep; ZK337.1b; CE16719.

InterPro; IPR002890; AZM N.

InterPro; IPR000847; HTH_Lyss.

InterPro; IPR001899; WacrogloblnA2.

InterPro; IPR001917; NHtransf_2.

Pfam; PF00207; AZM; 1.

Pfam; PF00207; AZM; 1.

Pfam; PF01835; AZM, N; 1.

PFOSITE; PS000599; ĀA TRANSFER CLASS 2; 1.

PROSITE; PS00477; ALPHA 2 MACROGLOBULIN; 1.

PROSITE; PS00444; HTH_LYSR_PAMILY; 1.

PROSITE; PS000474; HTH_LYSR_PAMILY; 1.

Alternative splicing; Hypothetical protein.

VARSPLIC 714 724

VARSPLIC 714 724

SEQUENCE 1519 AA; 160385 MW; 78139ACB56
                                                                                                                                                                                                                                                       EMBL;
EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 168.4 kDa protein ZK337.1.
ZK337.1.
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Rhabditidae; Pelode;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                             Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ZK337.1B (SHOWN H
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O46015; O46014;
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                                                                                                                                                                                                                                                   - ALTERNATIVE PRODUCTS: 2 ISO ZK337.1A; ARE PRODUCED BY A MBL; Z82090; CAB05007.1; -. MBL; Z82090; CAB05006.1; -. SSP; P01024; 1C3D.
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477; Conserv
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                 25.2%;
31.6%;
290;
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                                                        etical protein.
MISSING (IN ISOFORM ZK337.1A).
MW; 78139ACB564AB742 CRC64;
                 Pred.
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  Mismatches
 1850; DB 5;
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ismatches 563;
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VCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVSVL

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                                                                                                 KDYIDGVYDNAEYAERFMEENEGHIVDIHDFSLGSS----PHVRKHFPETWIWLDTNMGYR
                                                                                                                                                                                                                                                                                                                                                                                                          AVSPTKSFLQLLADNEGAVDVGKSLSFSLKATQPLSTITYQVMSRSNIVVSQQMTVNSEH
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HHAKQYAFVDPNVISRAVAFLNSQQMESGAFAERGEVHHKDMQGGAQDGGVALTAFVLIS
                                                                                                                               AVYFPIVPSSIGEIPVHISAIASQGGDAVEMNLRVDPQGYKVDRNIPFVIDLNNNSSDFS
                                                                                                                                              -VLFPIRPTHLGEIPITVTALSPTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQST
                                                                                                                                                                         ALLVLVFNYMEKEQDVTVTLKYDKDSGYDLLKKDGTVVRRDEVGQQNVRIVSVAGGGTSK
                                                                                                                                                                                              ALEITIFNYLKDATEVKVII--EKSDKFDILMTSSEI---NATGHQQTLLVPSEDGAT--
                                                                                                                                                                                                                                                               VMMMDGAPGMAEAA--FAAPPMG-----GSSPPPPTVRKFFPHTWIWSDLN-STS
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           LEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDPGRVIHSELQGG-NKSPVTLTAYIVTS
                                                                                     -KNILELIMPNDVVDGSQXARLDVIGDNMGPVLNNAHKLVQMPYGCGEQNMLNLVPNILVV
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Q8T398 PRELIMINARY; PRT; Q8T3398; O1-JUN-2002 (TrEMBLrel. 21, Create 01-JUN-2002 (TrEMBLrel. 21, Last s 01-MAR-2003 (TrEMBLrel. 23, Last a Alpha-2-macroglobulin homologue.
                                                                                                                                                                                                                                                                                                                                                                                               Hammond J.A., Nakao M., Yano T., Kemp G.D., Smith V.J.;
"Complete CDNA of an alpha2 macroglobulin homologue with
histidine residue from Ciona intestinalis.";
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ431688; CAD24311.1; -.
InterPro; IPR001289; A2M N.
InterPro; IPR001599; MacrogloblnA2.
InterPro; IPR001599; MacrogloblnA2.
InterPro; IPR00184; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ciona intestinalis.
Eukaryota; Metazoa; Chordata; Urochordata;
Phlebobranchia; Cionidae; Ciona.
                                                                                                                                                                                                                                             Pfam; PF00207; A2M; 1.

Pfam; PF01835; A2M N; 1.

SMART; SM00209; TSP1; 1.

PROSITE; PS00477; ALPHA 2 MACROGLOBULIN; 1.

PROSITE; PS00225; CRYSTALLN BETAGAMMA; 1.

PROSITE; PS00225; TSP1; 1.

PROSITE; PS00925; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Hepatopancreas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7719;
                                                                                                                                                          al Similarity
453; Conserv
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                                                                       LLATLSSLATASNV-YNIYFPKHIRPGFNISFTAAIIDN-PNTVQIHTAFRSMDNSFHVD
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%; Pred. No. 2.3e-99;
293; Mismatches 586;
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NARIYLENHLT-SISDNKYALAIVTYALHVAGSSRANEALLALEALATVQGGFKFWHDNS
                                   ----FLESEFSRGISDN-YTLALITYALSSVGSPKAKEALNMLTWRAEQEGGMQFW----V
                                                                                                           YTWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIH
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                                                                                                                                                                              FQTGYSNELNYKHRDGSFSAFGEGDASGSTWLTAFAAKCFMFARELRPTL-VSASVIDQA
                                                                                                                                                                                                                           MRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCFL---EADPYIDIDQNVLHRT
                                                                                                                                                                                                                                                                                              EVDAVLTLTESNKFVLLRPGNNSAAVGFSRRITIPASGSVSVKFPIRMGTLGEIPITMTA
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RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Champe M., Pfeiffer B.D.,
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Cherry J.M., Cawley S., Dahlke C., Davemport L.B., Davies P.,
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RA Dorbin K., Evangelista C.C., Ferraez C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
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RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
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Eukaryota; /
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo:
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                TPTVKDTENQLLIVD--VCAEYVPLEDADKDKDSNMAVMEIALPSGFVGDSTSLGKIQA
                                                                                                                                UNPENSLYLQTHDLPKSTRKVDFTAKGTGSAMVQLSYRYNLAEK-----EKKPSFK
                                                                                                                                                                                                                                                                                                                        VLLAFFENHELIPKYQSAIKKAVRYVAEEADK-TDDQYSLAIAAVALQLAKHPQSEKVIA
                                                                                                                                                                                                                                                                                                                                                                                                          VLRCFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLQSTLKTLSFSFPPNTVTGSERVQITAIGDVLGPSINGLASLIRMPYGCGEQNMINFAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEDGATVLFPIRPTHLGEIPITVTALSPTASDAVTQMILVKAEGIEKSYSQSILLDLTDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKRGEVIAIPVVIFNYLDKTLDADVVMDNSDQEYEFTEATNEVLEKAIDEVRRVKRVTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIRGEEFALEITIFNYLKDATEVKVIIEKSD-KFDILMTSSE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYTVPQS----GTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFK-SP-SKTYIQLKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HFEANKSFIYQVVVKNVDGSPVT--NSAKNVKIGF-DKSYSYFHEPSPK-
    VDRVKRVETKNSDSTVVVYFDSLTPGDVRCLPLEASKAHAVAKQKPASVSLYDYYDTERK
                                 SETVKKVEYDH--GKLNLYLDSVNETQF-CVNIPAVRNFKVSNTQDASVSIVDYYEPRRQ
                                                                                                                                                                                                                             GIPIMRWLSRORNSLGGFASTODTTVALKALSEFA--ALMNTERTNIQVTVTGPS-----
                                                                                                                                                                                                                                                                                            MLTWRAEQEGGMQFWVSSESKLSDS
                                                                                                                                                                                                                                                                                                                                                        IVTSLLGYRKYQPNID--VQESIHFLESEFSRGISDNYTLALITYALSSVGSPKAKEALN
                                                                                                                                                                                                                                                                                                                                                                                        VMRSFHQAGTYTDIDPKVITAGLDFLVSKQKESGEFPEVGKL----FDNANQNPLALTSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANSGKSVSFMIRPKNVGFTTLKITATSALAGDAIHQKLKVEPEGVTLFENRAVFINLKDQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPKATIYVYYVVNN-DLQFEEKTIDFEKEFSNSIDVS-APTNAKPSEEVKLRIK-TDADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTKKPRLGEQVSFDVVSIEDLPYFVYTIVARGNVILSDYVDVPDGQKTYTV-KFTPTFSM
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                                                                                                  LDVAVKENKDDLNHVDLNVCTSF----
                                                                                                                                                              -SPSPLAVVQ-----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFD
                                                                                                                                                                                                                                                             KLESVARKENDRMWW----SKATESTGEDGRVFHWKPRSNDVEITSYVLLALLEKDPAEK
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                                                                                                SGPGRSGMALMEVNILLSGFMVPSEA---
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RA Ballew R.M., Basul A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Ferriara S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Goong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McShrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mullians S.M., Moly M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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RA Yellams S.M., Woolage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
"The genome sequence of Drosophila melanogaster.";
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Than C.,

RA Yellams S.M., Washing M., Washing G., Zhao Q., Zheng L.,

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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
Example R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mixlos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
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Best Local :
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Pfam; PF01835; A2M N; 1.
PROSITE; PS00477; ĀLPHA 2.
PROSITE; PS00284; SERPIN;
SEQUENCE 1397 AA; 15510
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InterPro; IPR002890; !
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Submitted (MAR-2000)
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M., Drysdale R.,
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NFEAPVNENGIATENVRLPD-SDSRYYRIFASFDGSENTIGSISKFEPTPMSREPLKIQV
                          NYTVPQS----GTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFK-SP-SKTYIQLKT
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                                                                               VLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQKI
                                                                                                              --IIHWAQRG--QYLP----PIKLFAVVTEELTGNKQNATATVVLHQQRYSIEPYERPE
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J.S., Prochnik S.E., Smith C.D.,
,, Carlson J.W., Celniker S.E.,
,, Frise E., de Grey A., Harris N.,
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                                                                                                                                            ERKATEYY - - QVKSSLCDICEGADCGEGCK
                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -SPSPLAVVQ-----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQE
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       RX MEDLINE 2019606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Beeson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Compley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Geblos B., Delcher A., Dang Z., Mays A.D., Dev J., Dietschman W.,
RA Geblos B., Delcher A., Deng Z., Mays A.D., Dev J., Davies P.,
RA Geblos B., Delcher A., Deng Z., Mays A.D., Dev J., Davies P.,
RA Geblos B., Delcher A., Davies P., Seriza C.,
RA Harris N.L., Harvey D., Heiman T.J., Herrandez J.R., Houck J.,
RA Harris N.L., Harvey D., Keiman T.J., Herrandez J.R., Houck J.,
RA Globe P., Calley R., Karvitz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Keiman T.J., Herrandez J.R., Houck J.,
RA Harris N.L., Harvey D., Keitt C., Kravitz S., Kulp D., Lai Z.,
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                                                                                                           RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., Busans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., A Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A., Racalson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., Perriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., A McIntosh T.C., Moy M., Murphy B., Nelson C., Melson K.A., Nunco J., Marticosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Stapleton M., Strong R., Svirskas R., Tector C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Misra S., Crosby M.
Hradecky P., Huang
Tupy J.L., Bergman
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo:
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                       SEQUENCE FROM N.A.
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    Bayraktaroglu L., Cau
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EMBL; AE003618; AAN1
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|||:|||| || :||: ::::| | .::::| | .::
| SVFVQTDKATYKPADLVQFRILFLDENTRPAKIEKPISVIIIDGAQNRIKQLSDVKLTK
                                                                                                                                                                                                                                                                                                            HFEANKSFIYQVVVKNVDGSPVT--NSAKNVKIGF-DKSYSYFHEPSPK-----TRI
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                                                                                                                                                                                                                                                                                                                                                              --IIHWAQRG--QYLP----PIKLFAVVTEELTGNKQNATATVVLHQQRYSIEPYERPE
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                                                                                                  TPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDS
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                                                                                                                                                       VPKATIYVYYVVNN-DLQFEEKTIDFEKEFSNSIDVS-APTNAKPSEEVKLRIK-TDADS
                                                                                                                                                                                                                                                                                   NYTVPQS----GTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFK-SP-SKTYIQLKT
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ADVWIW--QSIGRSVGEEEFTLTKKIPDTITSWVVTGFSLNPTSGIALTKNPSKIRVFQP
                         PETWIWLDTNMGYRI-YQEFEVT--VPDSITSWVATGFVISEDLGLGLTTTPVELQAFQP
                                                                          AN--LTKDYIDGVYDNAE-YAERFMEENEGHIVDIHDFSLGSSP-----HVRKHF
                                                                                                                                                                                                       NTKKPRLGEQVSFDVVS1EDLPYFVYTIVARGNVILSDYVDVPDGQKTYTV-KFTPTFSM
                                                                                                                                                                                                                                 RDENIKVGSPFELVVSGNKRLKELSYMVVSRGQL-----VAVGKQNSTMFSLTPENSW
                                                                                                                                                                                                                                                            NFEAPVNENGIATFNVRLPD-SDSRYYRIFASFDGSENTIGSISKFEPTPMSREPLKIQV
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293; Mismatches 541; Indels 182;
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e EMBL/GenBank/DDBJ d
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101-OCT-2000 (TrEMBLrel. 15, Created)
1 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
1 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
1 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
2 TEP2 protein precursor (CG7052 protein) (GH01829p).
2 TEP1I OR TEP2 OR CG7052 OR CG18589.
3 Drosophila melanogaster (Fruit fly).
4 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Eukaryota; Endopterygota; Diptera; Brachycera; Muscon Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                      Q9NFV7
                                                     Lagueux M., Perrodou E., Levashina E.A., Capovilla M., I
"Constitutive expression of a novel complement-like prot
and Jak gain-of-function mutants of Drosophila.",
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
  MEDLINE=20196006; PubMed=10731132
               SEQUENCE FROM N.
STRAIN=Berkeley;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galler,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Harandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,
RA Haris H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Pandrews-Frannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottiter P.,
RA Bortis K.C., Blazen J.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.B., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dotson K., Doup L.B., Downes M., Dugan-Rocha S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lii X.,
RA Liux X., Mattei B., McIntosh T.C., McLeod M.P., McBherson D.L.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lii X.,
RA Mount S.M., Murphy B., Murphy L., Murny D.M., Nelson K.A., Nixon K., Nuxsherm D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Pari V., Reese M.G.,
RA Mount S.M., McMander R., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier S., Waysarri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
The Spier E., Spradling R., Rogher S
RA CeIniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A., and Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y., RA Banzon J., An H., Baldwin D., Banzon J., Besson K.Y., Busam D.A., Rallson J.W., Center A., Champe M., Davenport L.B., Dietz S.M., Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D., A., Perriera S., Frise E., Galle R.F., Garg N.S., George R.A., Gonzalez M., Houck J., Hoskin R.A., Hostin D., Howland T.J., A., Hostin D., Howland T.J., A., McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Pfiffer B., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Stapleton G., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; "Sequencing of Drosophila melanogaster genome.";
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Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                           Venter C.J.;
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InterPro; IPR002890; A2M N.
InterPro; IPR001599; MacrogloblnA2.
InterPro; IPR000215; Serpin.
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Pfam; PF01835; A2M_N;
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EMBL; AE003618; AAF52541.2;
EMBL; AY122084; AAM52596.1;
HSSP; P01024; 1C3D.
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Pred. No. 3.
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V., Park S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALMEVNLLSGFMVPSEA---ISLSETVKKVEYDH--GKLNLYLDSVNETQF-CVNIPAVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGSGSGTMDIEFSSAGESKNTIKVNPENSLVLQTHDLPKSTRKVDFTAKGTGSAMVQLSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RSNDVEITSYVLLALLEKDPAEKALPIIKWLISQRNSNGGFSSTQDTVIGLQALTKFAYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EATNEVLEKAIDEVRRVKRVTIPANSGKSVSFMIRPKNVGFTTLKITATSALAGDAIHQK
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                                                                                                           (Fruit fly).
                                                                                                                                                                                       Last sequence up
                                                                                                                                                                                                                                          Created)
                                                                              Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                    update)
                                                        Muscomorpha;
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     RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brill J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayrakrargju L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Davies S., Fleischmann W.,
RA Cherry J.M., Cawley S., Davies S., Fleischmann W.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Cawley S., Cawley R.,
RA Cherry J.M., Cawley S., Cawley S., Cawley R.,
RA Cherry J.M., Cawley S., Cawley L.,
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RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragas V., Park S., Patel S., Pfelfer B.,
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Phouanenavong S., Pittman G.S., Furi V., Richards S., Scheeler F.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
"Sequencing of Drosophila melanogaster genome.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                           Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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        S.E.,
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PROSITE;
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Pfam; PF01835; A2M; 1.
PROSITE; PS00477; ĀLPHA 2 MACROGLOBULIN;
PROSITE; PS00284; SERPIN; 1.
SEQUENCE 1399 AA; 155783 MW; 3D8B7DF9
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InterPro; IPR001599; MacrogloblnA2
InterPro; IPR000215; Serpin.
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                                                                                                                                                                               VPKATIYVYYVNN-DLQFEEKTIDFEKEFSNSIDVS-APTNAKPSEEVKLRIK-TDADS
                                                                                                                                                                                                          TPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDS
                                                                                                                                                                                                                                        NTKKPRLGEQVSFDVVSIEDLPYFVYTIVARGNVILSDYVDVPDGQKTYTV-KFTPTFSM
                                                                                                                                                                                                                                                            RDENIKVGSPFELVVSGNKRLKELSYMVVSRGQL-----VAVGKQNSTMFSLTPENSW
                                                                                                                                                                                                                                                                                                            NYTVPQS----GTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFK-SP-SKTYIQLKT
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                                                                                           ANLTKDYIDGVYDNAEYAERFMEENEGHIVDIHD--FSLGS-----SPHVRKHFPETW
                                                                                                                           FVGLLGVDQSVLLLKSGNDLSQDDIFNSLNIYQTS---TPWMNGYGRYPGQTSGLVTLTN
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                                                                                                                                                                                                                                                                                                                                                                                                      --IHWAQRG--QYLP-----PIKLFAVVTEELTGNKQNATATVVLHQQRYSIEPYERPE
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               IFNIFENVG---EEEFTLTKKIPDTITSWVVTGFSLNPTSGIALTKNPSKIRVFQPFFVS
                                         IW-LDTNMGYRIYQEFEVT--VPDSITSWVATGFVISEDLGLGLTTTPVELQAFQPFFIF
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                                                                      YPYNTERRIFIRPGIGFPRPLFNRVTVAGSLPPNVIPEPQVRKEFPENW
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AC 00171
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01-JUL-1997
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               InterPro;
InterPro;
                                        MEDLINE=97175055; PubMed=9022715;
Iwaki D., Kawabata S., Miura Y., Kato A., Armstrong P. Quigley J.P., Nielsen K.L., Dolmer K., Sottrup-Jensen "Molecular cloning of Limulus alpha-2-macroglobulin.";
Bur. J. Biochem. 242:822-831(1996).
EMBL, D83196; BAA19944.1; -.
HSSP; P01024; 1C3D.
                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Limulidae; Limulus. NCBI_TaxID=51645;
                                                                                                                                     SEQUENCE FROM N.A.
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; IPR002048;
; IPR001599;
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Pfam; PF01835; A2M X; 1.
PROSITE; PS00477; ĀLPHA 2 MACROGLOBULIN; 1.
PROSITE; PS00018; EF HAND; 1.
PROSITE; PS00018; EF HAND; 1.
SEQUENCE 1507 AA; 168490 MW; 8EF4013495F63CED
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Q9ULD7;
01-MAY-2000
01-MAY-2000
01-MAR-2003
                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                          SSUE=Brain;
                                                                                                                                                   large proteins in vitro. Res. 6:337-345(1999).
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                                                                                                                     P01024; 1C3D
                                                                                                                                       AB033109; BAA86597.1;
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RTYTWLKGHQKSNGEFWDPGRVIHSELQGG----NKSPVTLTAYIVTSLL--GYRKYQPN
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                                                                                                                                                                                                                                   RGGFYSTQDTVIALQAMSKFATIIYKDELDLEVGVESSGFEKKIMLTKDNSILMQTFRLQ
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                                                                                                                                                        TVPSPVDFEATGSGCGLVQTSLRYNVNTP-----PPRKGFHLEVTVKRGLYRDCIN
                                                                                                                                                                                                                                                                                                                                                  EGGMQFWVSSESKLSDSWQPRSLDIEVAAYA---LLSHFLQFQTSEGIPIMRWLSRQRNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TENWILNRQRSNGCFRKIGKLFNSALKGGISSNDETPAPLTAYVLISLLEAGYKN----
                                                                                                                                                                                            -PMAVNISANGEGEAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVKEN--KDDLN
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InterPro; IPR002890; A2M_N.
InterPro; IPR002350; kazal.
InterPro; IPR001599; MacrogloblnA2.
Pfam; PF00207; A2M; 1.
Pfam; PF00805; A2M_N; 1.
Pfam; PF00050; kazal ; 1.
SMART; SM00280; KAZAL; 1. ul-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein KIAA1283 (Fragment).
KIAA1283. MEDLINE=20039619; PubMed=10574462; Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., "Prediction of the coding sequences of unidentified human The complete sequences of 100 new cDNA clones from brain v Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo. 1884 ₿ Nomura N., mura N., Ohara O. d human genes. XV brain which code

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Hypothetical protein.
NON TER 1 1
SEQÜENCE 1884 AA; 206524 MW; D3C078F;
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  832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELLKTASNLTVSVLEAEG-VFEKGSFKTLTLPSLPLNSADEIYELRVTGR---TQDEILF :|: | : : | : : |
 TCAEVYMKLSVPKGIQF
                                                                          SITSWVATGFVISEDLGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLK 775
                                                                                                    AFQPHTGSLV----AVAPSRHPPRTEKRKRTFFPETWIWHCLNISDPSGEGTLSVKVPD
                                                                                                                                                                      -----YLGMFMNSFAVFQECGLWVLTD-ANLTKDYIDGVYDNAEYAER
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                                                                                                                                                                                                                                    VSLRISVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTG------
                                                                                                                                                                                                                                                            SLHLAVTP--SMVPLGRLLVFYVRENGEGVADSLQFAVETFFENQVSVTYSANETQPGEV 600
                                                                                                                                                                                                                                                                                STMFSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEK
                                                                                                                                                                                                                                                                                                                 LYYEVAARGNIVLSGQQPAHTTQQRSKRAAPALEKPIRLTHLSETEPPPAPEAEVDVCVT
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                        DATEV--KVIIEKSDKFDILMTSSEINATGH-----QQTLLVPSEDGATVLFPIRPTHL
                                                                                                                              FMEENEGHIVDIHDFSLGSSPH------VRKHFPETWIWLDTNMGYRIYQ-EFEVTVPD
                                                                                                                                                        WAGLTAQRRRRSSVFPWPWGITKDSGFAFTETGLVVMTDRVSLNHRQDGGLY--TDEAVP
                                                                                                                                                                                                          VDLRIRAAR-GSCVCVAAVDKSVYLLRSGFRLTPAQVFQELEDYDVSDSFGVSREDGPFW
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RESULT 14
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ID Q8IZZ-
AC Q8IZZ-
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-M2
DT 01-M2
DT 04-M2
DT 04-M2
DC Mamma
OC Mamma
OX NCBI
QBIZJ3 PRELIMINARY; PRT; 1885 AA.
QBIZJ3;
Q1-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Alpha-2 macroglobulin family protein VIP.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E--SLEQLILDKHMGMKRYEVAGRRVLFYFDEIPSRCLTCVRFRALRECVVGRTSALPVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----AFDLDVAVKENKDDLNHVDLNVCTSFSGPGRSGMALMEVNLLSGFMVPS
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SEQUENCE
Li Z., Wu
"Cloning
member.";
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                    774
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Wu X., Engvall E.
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                                                SITSWVATGEVISEDIGIGITTTEVELQAFQPFFIFLNIPYSVIRGEEFALEITIFNYLK 775
                                                                                                                                                                                                                                                                                                                                                             LSYMVVSRGQLVAVGKQ-----N
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                   SITSWVGEAVALSTSQGLGI-AEPSLLKTFKPFFVDFMLPALIIRGEQVKIPLSVYNYMG
                                                                                                                                             WAGLTAQRRRRSSVFPWPWGITKDSGFAFTETGLVVMTDRVSLNHRQDGGLY--TDEAVP
                                                                                                                                                                                                                                      VSLRISVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTG-------
                                                                                                                                                                                                                                                                     SLHLAVTP--SMVPLGRLLVFYVRENGEGVADSLQFAVETFFENQVSVTYSANETQPGEV 601
                                                                                                                                                                                                                                                                                                  STMFSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEK 573
                                                                                                                                                                                                                                                                                                                              LYYEVAARGNIVLSGQQPAHTTQQRSKRAAPALEKPIRLTHLSETEPPPAPEAEVDVCVT
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                                                                                                             FMEENEGHIVDIHDFSLGSSPH-----VRKHFPETWIWLDTNMGYRIYQ-EFEVTVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FDICVRDM-----IPADVPEHFRGRVSIWAMVT-SVDGSQQ------
                                                                                                                                                                                                      VDLRIRAAR-GSCVCVAAVDKSVYLLRSGFRLTPAQVFQELEDYDVSDSFGVSREDGPFW
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                                                                                                                                                                        ----YYLGMFMNSFAVFQECGLWVLTD-ANLTKDYIDGVYDNAEYAER
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RESULT 15

G00486

ID Q60486;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MOV-2003 (TrEMBLrel. 23, Last annotation update)
DE Alpha-macroglobulin precursor.
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1705	17.1	1411	1645	1364	1587	1312	1528	1263	1476	1217	1416	1181	1356	1137	1302	1077	1242	1019	1182	959	1122	899	1062	883	1002	874	942	863	882	828	833	776
AAI 1707		SVT 1413	VYDYYEPAFEATREYNVSTHSPLARELCAGPACNEVERAPARGPGWFPGESGPAVAPEEG 1704	IVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHHS 1410	ESLEQLLLDKHMGMKRYEVAGRRVLFYFDEIPSRCLTCVRFRALRECVVGRTSALPVS 1644	Αĭ	AAEGSRGDWPPADDDDPAADQHHQEYK-VMLEVCTRWLHAGSSNMAVLEVPLLSGFRADI 1586	AFDLDVAVKENKDDLNHVDLNVCTSFSGPGRSGMALMEVNLLSGFMVPS 1311	GLFVSAKGDGCCLMQIDVTYNVPDPVAKPAFQLLVSLQEPEAQGRPPPMPAS 1527	PLAVVQPMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQE 1262	TODTCVALQALAEYAILSYAGGINLTVSLASTNLDYQETFELHRTNQXVLQTAAIPSLPT 1475	TQDTTVALKALSEFAAL	VDKGTFLSFSDRVSQSVVSAEVEMTAYALLTYTLLGDVAAALPVVKWLSQQRNALGGFSS 1415	PRSLDIEVAAYALLSHFLQFQTSEGIPIMRWLGRQRNSLGGFAS 1180	SAAPLAM-DPYSCALTTYALTLLRSPAAPEALRKLRSLAIMRDGVTHWSLSNSWD 1355	SEFSRGISDNYTLALITYALSSVGSPKAKEALNMLTWRAEQEGGMQFWVSSESKLSDSWQ 1136	QQQADGSFLAVGRVLNKDIQGGIHGIVPLTAYVVVALLETGTASEEERGSTDKARHFLE 1301	GHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLE 1076	QYQRQLTYKRQDGSYSAFGERDASGSMWLTAFVLKSFAQARSFIFVDPRELAAAKSWII 1241	QGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLK 1018	IIGDVMGPTLNHLNNLLRLPFGCGEQNMIHFAPNVFVLKYLQKTQQLSPEVERETTDYLV 1181	AIGDVLGPSINGLASLIRMPYGCGEONMINFAPNIYILDYLTKKKQLTDNLKEKALSFMR 958	VAWTLPRPPEVQFIGFSTGWGSMGEFRIWRKMEVDESYSEAFTLGVPHGAIPGSERATAS 1121	SFPPNTVTGSERVQIT 898	LGGHQNTRSWISTSKMGEPVASAHTAKILSWDEFRTFWISWRGGLIQVGHGPEPSNESVI 1061		SAFFCPSERVHISTPNKYEFQYVQRPLRLTRFDVAVRAHNDARVALSSGPQDTAGMIEIV 1001	SIL	GLNNITAKALAYGDTNCCRDGRSSKHPEENHADRRVPIGVDHVRRSVMVEAEGVPRAYTY 941	GEIPITVTALS	TCAEVYMKLSVPKGIQFVGHPGKRHVTKKMCVAPGEAEPIWVVLSFSDL 881	DATEVKVIIEKSDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHL 827

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SIGNAL
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EMBL; D84338; BAA12316.1; -.
HSSP; P01023; 18V8.
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PROSITE; PS00477; ALPHA 2 MACROGLOBULIN; PROSITE; PS00430; TONB_DEPENDENT_REC_1;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Pred. No. 6.7e-82;
12; Mismatches 524;
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AIAEYHA 1467
                          AVRSYNS 1380
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arch completed: January 15, 2004, 18:14:03 b time : 64 secs

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Minimum DB
Maximum DB
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-MCDEL=frame+_p2n.model -DEV=xlp
-MCDEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US10020095/runat_15012004_163822_18713/app_query.fasta_1.1607
-DB=EST -QFMT=fastap -SUFF1X=rst -MINATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_NIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MIXLEN=200000000
-USER=US10020095_@CGN_1_1 4337 @runat 15012004_163822_18713 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRANS=1 -XGAPDP=10 -XGAPDXT=0.5 -FGAPOP=6
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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ALIGNMENTS

ACCESSION	LOCUS DEFINITION	RESULT 1

VERSION KEYWORDS SOURCE ORGANISM AK029247

AK029247

AK029247

Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4031440K17 product:weakly similar to alpha-2-macroglobulin (fragments) [Limulus polyphemus], full insert Mus musculus (house mouse) AK029247 AK029247.1 GI:26081244 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; HTC; CAP trapper. sequence.

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REFERENCE
AUTHORS
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                                                        Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P. Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiramoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Munazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Interest Cummantsu, M. and Hayashizaki, Y.
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute
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Please visit our web site for further details.
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LysProLysG1nG1uVa1LysPheArgI1eVa1ThrLeuPheSerAspPheLysProTyr
                                                                                                                  ArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeuTyr
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weakly similar to alpha-2-macroglobulin (fragments)
(Limulus polyphemus) (PIR|A36260, evidence: FASTY,
51.8%ID, 76.7%length, match=168)"
a 970 c 1010 g 1228 t
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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/mol_type="mRNA"
/strain="C57BL/6J"
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Db 2619 ACGCTGCCTCACCCACTGCTCTCATGCTTCACCAACAATTGTAGTAAAGCCTGAA 2678 Qy 855 GlylleGluLysSerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuGln 874	ThralaeuSerProThralaSerAspAlaValThrGlmMetIleEuValLyshlaGlu	795 TH 2499 AC 815 CI	Qy 775 LysAspAlaThrGluValLysVall1eIleGluLysSerAspLysPheAspIleLeuMet 794	Qy 755 ProTyrSerVallleArgGlyGluGluPheAlaLeuGluIleThrIlePheAsnTyrLeu 774	Qy 735 LeuThrThrProValGluLeuGlnAlaPheGlnProPhePheIlePheLeuAsnLeu 754	Qy 715 AspSerIleThrSerTrpValAlaThrGlyPheValIleSerGluAspLeuGlyLeuGly 734	3-1	IleHisAspPheSerLeuGlySerSerProHisValArgLysHisPheProGluThrTrp	はニザ		615 GluLeuTyrAsnThrGlyTyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGln 	Qy 595 SerValAsmLeuMetAsmAlaSerAsmAspIleThrMerGluAsmValValHisGluLeu 614	575 SerLeuArgileSerValThrGlnBroAsgSerIleValaltyIleValAlaValAspLys	55 PhelyskanlyslielysleuTyrTrpSerlysVallysAlaGluProSerGluLysVal ::: ::: 1779 TTTGAAAATAAGGTAAAGCTGTTTTGGAGTAAACCTACAGTCAAGCCATCTGATAAGGTC	1719 TATATIGCAGAGGATGGGGAAATTATAAATGATATCTAAAAATCCCCGTTCAGCTTGTT	515 ThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysVallleValTyr

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 LeuAlaValValGlnProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIle 1237
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                               CCCAGATCCATACACTTCCGAATTGACTCCCAGAACCTCTTTCTCCTTCACCAGGAAGAG
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Shibata, K.,

Itoh, M.,

Aizawa, K.,

Nagaoka, S.,

Sasaki, N.,

Carninci, P.,

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AK036799
AK036799.1
HTC; CAP
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                         Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999) 99279253
                                                                                                                                                                                                                                                              Mus
                                                                                                                                                                                                                                                                                                                                                                AK036799 4725 bp mRNA linear HTC (Mus musculus adult female vagina cDNA, RIKEN full-length library, clone:9930012E15 product:weakly similar to alpha-2-macroglobulin (fragments) [Limulus polyphemus],
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Rodentia;
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                                                                                                                                                                                                                                                                                              Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishire,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                             prepare mouse tissues.

Please visit our web site for further
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                           URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
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551 lGlnLeuValPheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSe 571 ::: ::: :::	531 lileValTyrTyrTleGluAspAspGlyGluIleIleSerAspValLeuLysIleProVa 551	511 gGlnasnSerThrMetPheSerLeuThrProGluAsnSerTrpThrProLysAlaCysVa 531 :::	491 sArgLeuLysGluLeuSerTyrMetValValSerArgGlyGlnLeuValAlaValGlyLy 5 :::: :::	471 sThrArgAspGluAsnIleLysValGlySerProPheGluLeuValValSerGlyAsnLy 491 	85erSerMetAlaValHisSerLeuPheLysSerProSerLysThrTyrIleGlnLeuLy 471	1 uPheProIleLeuGluAspSerSerGluLeuGlnLeuLysAlaTyrPheLeuGlySerLy 45	1 sMetGluhlaValGlnLysIleAsnTyrThrValE 	1 ThrGlnArgAsnTyrThrGluTyrTrpSerGlySerAsnSerGlyAsnGlnLy 41	4 ArgAlaAspGlyAsnGlnLeuThrLeuGluGluArgArgAsnAsnValValIleThr-Va 	354 PheAspTyrThrThrValLeuLysProSerLeuAsnPheThrAlaThrValLysValThr 	334 IleSerArgAsnValSerThrAsnValPhePheLysGlnHisAspTyrIleIleGluPhe 353 114 ATCTCAAGAATGGCAACCAATGTGTTTTTCAAGCAACATGATTACATCATTGAGATT 1173	4 4	0 4	280 IleThrLysThrPheLysIleAsnGlySerAlaAsnPheSerPheAsnAspGluGluMet 299 ::: :::	260 llysGly-AspValThrLeuThrPheLeuProLeuSerPheTrp-GlyLysLysLysAsn 279 ::::::	241 MetAønSerLy8Hi9LeuAønGlyThrIleThrAlaLy8TyrThrTyrGlyLy8-ProVa 260 ::: :::::	221 ValSerGluTyrValLeuProLysPheGluValThrLeuGlnThrProLeuTyrCysSer 240	694 TTTGGTGACTGGTCCATTCAGGTTCAAGTGAATGATCAGCAATATTACCAGTCATTTCAG 753
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                                 ACGGAGATCTACCGAAAATCAAGAAGTTTTTGATTTAGACGTCATTGTG----AATAATGA
                                                              gArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLy
                                                                                                                                                                   CCAGGAAGAGCTTCATGCGCTAGATCCCCATCACCGTTAATGTTTCTGCGCATGGCTCGGG
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Contact: XGC help desk
Email: cgapbs -r@mail.nih.gov
Tissue Procurement: Dr. Igor Dawid
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Brin Helton, Mark Kettem
Madan, Stephanie Rodrigues, Amy Sanchez and Michell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (13-JAN-2003) National Institutes of Health, Xenopus Gene Collection (XGC), National Institute of Child Health and Human Development, 6100 Executive Boulevard, Room 4B01, Rockville, MD
                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 94 Row: b Column: 12

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein This clone has the following problem: frame shifted.
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BC044072
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1 (bases 1 to 4641)
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/organism="Xenopus
/mol_type="mRNA"
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                LysAsnValMetAspSerSerAsnGlyLeu-----
                                                GTCGATGTGTGCCGGAAGCATTACAGCTACAGAAGGGCATTTGGTAATGACAAAGGGAGA
                                                                               IleAsn---GlySerAlaAsnPheSerPhe----
                                                                                                                                           LeuThrPheLeuProLeuSerPheTrpGlyLysLysLysAsnIleThrLysThrPheLys
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/clone="IMAGE:4681494"
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CCAGTCAATGATTTTGGAAATTATGATTATCGGATTCAGGAAGCTGAGGATCACTGTCCA 2007
                                                                                                                            TCCCTACAAGTTCAGGCAGCT----GCCGGGTCTCTCTGTGGCCTGAGAGTGGTGGATAAG
                                                                                                                                                   SerLeuArgIleSerValThrGlnProAspSerIleValGlyIleValAlaValAspLys
                                                                                                                                                                                           TTTAGGAATAAGGTGTCAGTTGGCTTCTCCCCCAGATGAAGTTCTACCAGGATCAGATGTT 1830
                                                                                                                                                                                                                                                                                   TyrIleGluAspAspGlyGluIleIleSerAspValLeuLysIleProValGlnLeuVal
                                                                                                                                                                                                                                                                                                                       GTCTCCATCAAACTCAAGCTCAGTGTTGACGTCTCTCCGACTCTTCGAGTTCTGACCTAC
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                                                               AGTGTGGTGTTAATGAAACCTGACCAAGAACTGACGGCCGACAAGATTCGGGGACTCTTC
                                                                                           SerValAsnLeuMetAsnAlaSerAsnAspIleThrMetGluAsnVal------
                                                                                                                                                                                                                       PheLysAsnLysIleLysLeuTyrTrpSerLysValLysAlaGluProSerGluLysVal
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                               -----ValHisGluLeuGlu------
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	905 GlyProSerIleAsnGlyLeuAlaSerLeuIleArgMetProTyrGlyCysGlyGluGln 924 	885 ProProAsnThrValThrGlySerGluArgValGlnIleThrAlaIleGlyAspValLeu 904	2882 TGCTGCCAAGCTGGTGATCATCCTAAAACAGAGGAGATATCCCTTAAGGTC 2935		GlnMetIleLeuValLysAlaGluGlyIleGluLysSerTyrSerGlnSerIle	839ProThrAlaSerAspAlaValThr 846	823 ArgProThrHisLeuGlyGluIleProIleThrValThrAlaLeuSer	803 GlyHisGlnGlnThrLeuLeuValProSerGluAspGlyAlaThrValLeuPheProIle 822	783 IleIleGluLysSerAspLysPheAspIleLeuMetThrSerSerGluIleAsnAlaThr 802 	763 GlupheAlaLeuGluIleThrIlePheAsnTyrLeuLysAspAlaThrGluValLysVal 782 ::: ::: 2540 TCATTCGCTCTAAGGCACTGTCTTAACTACCTGAAGCAGTGTATAAAGGTTCAGACA 2599	743 GlnAlaPheGlnProPhePheIlePheLeuAsnLeuProTyrSerVallleArgGlyGlu 762 ::: 2480 CGAGTCTTCCAGCCCTTCTTTGTGGAGGTCCTCTGTCGTGCGTG	723 ThrGlyPheVallleSerGluAspLeuGlyLeuGlyLeuThrThrProValGluLeu 742	703 TyrArgIleTyrGlnGluPheGluValThrValProAspSerIleThrSerTrpValAla 722	686ValArgLysHisPheProGluThrTrpIleTrpLeuAspThrAsnMetGly 702	675 IleHisAspPheSerLeuGlySerSerProHis	657AsnAlaGluTyrAlaGluArgPheMetGluGluAsnGluGlyHisIleValAsp 674 ::: :::: ::::: 2188 GCCAGGGCTACCAGGACCTACTGGAGACCGAATGATTG-CATTTGCTTCCC 2246	640 ValLeuThrAspAlaAsnLeuThrLysAspTyrIleAspGlyValTyrAsp 656 :::::: :::::	620 GlyTyrTyrLeuGlyMetPheMetAsnSerPheAlaValPheGlnGluCysGlyLeuTrp 639 2068 CCATGGCATATGCCAGAGGAAGCTGATGTCTACGGCCTCTTCAAGAAAGTGCAACTAAAA 2127	616LeuTyrAsnThr 619 2008 TTCCGACCCTTTCCTTCCTTGGCGACCATTCAATAGAATTTCTAGATCCATTATATATCCC 2067
Q	Db 49	Db	Q B	& 8	\$ \$	p &	Qγ	Qγ σb	D Q	ОУ	Db	Оу	Db Cy) B Q	φq	D	₽ Q	Db Qy	Db Qy
1256 ArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLys 1274	1236 ATATLECYSGINLEUASNVALVALTYRASNVALLYSATASETGLYSETSERATGARGARG 1255	::: ::: :::::	3935 AAGACTGGATTCCATCAACAGTTCCATGTGGATCAAAATAACCGGCTCCTGCTACAGAAA 3994 1216 SerProLeuAlaValValGlnProMetAlaValAsnIleSerAlaAsnGlyPheGlyPhe 1235	1212 ProSerSerPro 1215	SerGluPheAlaAlaLeuMetAsnThrGluArgThrAsnTleGlnValThrValThrGly	1172 ArgAsnSerLeuGlyGlyPheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeu 1191 	LeuGinPheGlnThrSerGluGlyIleProIleMetArgTrpLeuSerArgGln ::: ::: TCTGGCCTCAAAAAGGACCTGGGGAAAAGCTTCTGAGATAGTCAACTGGCTGAGCAAGCA	SerTrpGlnProArgSerLeuAspIleGluValAlaAlaTyrAlaLeuLeuSerHisPhe :::	1118 GluGlyGlyMetGlnPheTrpValSerSerGluSerLysLeuSerAsp 1133	ValGlySerProLyBAlaLyBGluAla 		AsnIleAspValGlnGluSerIleHisPheLeuGluSerGluPheSer	1045 ProvalThrLeuThrA.aTyrileValThrSerLeuLeuGlyTyrArgLysTyrdInPro 1064 ::: ::: ::: ::: 3416 GAAACCTCTCTCTCTCTTATGTAACAATGGCTTTGCTA				LeuLeuTyrGlnArgGlnAspGlySerPheSerAlaPheGlyAsnTyrAspProSerGly	LeuThrAspAsnLeuLysGluLysAlaLeuSerPheMetArgGlnGlyTyrGlnArgGlu	AsnMetIleAsnPheAlaProAsnIleTyrIleLeuAspTyrLeuThrLysLysGln

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                                                                                  source
                                                                                                                                                                                               Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
more information about this cluster, see
http://www.genoscope.cns.fr/
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                                                                                               cgi-bin/cluster.cgi?seq=CSOBAI029ZD07_CS02740_1&cluster=3578.f. Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID: CSOBAI029ZD07_CS02740_1. Location/Qualifiers
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BP 191 91006 EVRY cedex - France
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1 (bases 1 to 941)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI081YB18"
                                                           organism="Homo sapiens"
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                                                                                    ThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThr
                                                                                                                                                                   GlyIleProIleMetArgTrpLeuSerArgGlnArgAsnSerLeuGlyGlyPheAlaSer
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                                                             ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA
                                                                                                                                            GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized.
a 214 c 181 g 266 t 9 others
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밁 Ś 밁 S 유성

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US-10-020-095-4 (1-1428) x AL554092 (1-1201) Qy	Alignment Scores: 7.4e-140 Length: 1201 Pred. No.: 1406.00 Matches: 293 Percent Similarity: 90.74\$ Conservative: 1 Best Local Similarity: 90.43\$ Mismatches: 29 Query Match: 19.13\$ Indels: 4 DB: Gaps: 1	/mol_type="mRNA" /db_xref="taxxon.960" /db_xref="taxxon.960" /clone="CSODIOBIYB18" /clone="CSODIOBIYB18" /clone="Lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="lat strand cDNA was primed with a NotI-oligo(dT) /note="lat strand cDNA was primed with a NotI-oligo(dT) /note="lat strand cDNA was primed with a NotI and cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized." BASE COUNT 359 a 238 c 236 g 293 t 75 others	Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3578.f For more information about this cluster, see http://www.genoscope.cns.fr/ cgi-bin/cluster.cgi?seq=CS0DI081DA09QP1&cluster=3578.f. Contact: Peng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 FEATURES Faraday Avenue Genoscope sequence ID: CS0DI081DA09QP1. Location/Qualifiers Location/Qualifiers formation about this cluster 3578.f. Contact: Location/Qualifiers Location/Qualifiers Location/Qualifiers	S EST. Homo sapiens sapiens Eukaryota; P Mammalia; Eu Mammalia; Eu Li, W.B., Gru RS Li, W.B., Gru RS Li, W.B., Gru On Feb 15.	SULT 5 554092 AL554092 AL554092 FINITION AL554092 Homo sapiens PLACENTA COT 25-NOR Clone CS0D1081YB18 5-PRIME, mRNA sequence CESSION AL554092.2 GI:31275905	Db 159 GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCTCTTGCTGTG 100 Qy 1221 ValGlnProMetAlaValAsnIleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeu 1240
DEFINITION Mus musculus, murinoglobulin 1, clone IMAGE:5097177, mRNA. ACCESSION BC049868 VERSION BC049868.1 GI:29437204 KEYWORDS HTC. SOURCE Mus musculus (house mouse) ORGANISM Mus musculus (house mouse) CORGANISM Mus musculus (house mouse) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; REFERENCE 1 (bases 1 to 4667) AUTHORS Strausberg,R. TITLE Direct Submission	991 AW-GIWAIGGAICI-ICAAAIGGACTTICIGAAACYKGGAIYIAIYI 321 ValGluIleLeu 324 1046 GIAGAAAITTTA 1057 168	261 LysGlyAspValThrLeuThrPheLeuProLeuSerPheTrpGlyLysLysLysLysAsmIle	Qy 181 Serd, Include Table Leuch Tyval Lieser Lystnrine Ginleuser Hisprolle 200 632 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCAATA 691 Qy 201 LeuGlyAspTrpSerIleGlnValGlnValAsnAspGlnThrTyrTyrGlnSerPheGln 220	452 ČĠĊŢTĀŢĊĀŢŢĠĀĠĀĊĊĀĀĠĀĠĀĀŢĀŢĊŢĠŢMŢŢĊĀŢŢĊĀĀĊĀĀĀĀĀĀĀĀĀĀ	Db 332 GAAAAARCTCTTTAARAWACTTAWTCTTCCATMAWTACMTCTGAACARTGAGATGAG 391 Qy 101 IleTyrGluLeuArgValThrGlyArgThrGlnAspGlulleLeuPheSerAsnSerThr 120	Db 212 AATGTGACTATTGGGGTGGAGCTTCTGGAAMACTGCCCTTMAMAGGTGACTGTGAAGGCG 271 Qy 61 GluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyValPhe 80

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Series: IRAK Plate: 99 Row: h Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6678965
This clone has the following problem: frame shifted:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: nisc_mgc@nhgri.nih.gov

Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Akhter,N., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.
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CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (31-MAR-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       web site: http://www.nisc.nih.gov/
                                                                            ValThrAlaProGlyIleIleArgProGlyGlyAsnValThrIleGlyValGluLeuLeu
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ACAGCTTCCTTGGTATCTCAATCAGGAAGGAAAAACCTGTTCGATGAGCTGGTGCTTGAC
                                      ThrValSerValLeuGluAlaGluGly-----
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1126 c 1046 g 1149 t
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/clone_lib="NCI_CGAP_Li9"
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/clone="IMAGE:5097177"
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                                                                                                                                                                                                                                                       ACAAACAAGCTCATA----
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                                                        AsnSerGlyAsnGlnLysMetGluAlaValGlnLysIleAsnTyrThrValProGlnSer
                                                                                                                                                                                                                                                                                                                                                                    ThrGluSerValThrGlyIle-----SerArgAsnValSerThrAsnValPhePheLys 345
                                                                                                                                                                                                                                                                                                                                                                                                            GAGCTCCAATCAAAGAAAAGGAATTATGAGGTTCAGCTTTTCCATGTGAATGCAACTGTT
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                                                                                                                                  ArgAsnAsnValValIleThrValThrGlnArgAsnTyrThrGluTyrTrpSerGlySer
                                                                                                                                                                           TTCTTTGTGAAAGTCCGCCTAGTGGATATCAAGGGAGACCCTATCCCAAATGAGAAA----
                                                                                                                                                                                                             PheThrAlaThrValLysValThrArgAlaAspGlyAsnGlnLeuThrLeuGluGluArg 385
                                                                                                                                                                                                                                                                                                                                    ACAGAAGAAGGGACAGGATTGGAGTTCAGTCGATCTGGAACAACTAAAATTGAAAGAATC 1104
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Oy 1032 rgVall1eHisSerGluLeuGlnGlyGlyAsnLysSerProValThrLeuThrAlaTyrI 1052 ::: :::::: ::::::::::::::::::::::::::	Qy 1012 rgThrTyrThrTrpLeuLysG1yHisGlnLysSerAsnGlyGluPheTrpAspProGlyA 1032	992 alleuArgCysPheLeuGluAlaAspProTyrIleAspIleAspGlnAsnValLeuHisA	Oy 974 heSerAlaPheGlyAsnTyrAspProSerGlySerThrTrpLeuSerAlaPheV 992	Qy 954 euSerPheMetArgGlnGlyTyrGlnArgGluLeuLeuTyrGlnArgGluAspGlySerP 974 ::	Qy 934 yrIleLeuAspTyrLeuThrLysLysLysGlnLeuThrAspAsnLeuLysGlnLysAlaL 954 :::	OY 914 euIleArgMetProTyrGlyCysGlyGluGlnAsnMetIleAsnPheAlaProAsnIleT 934	Qy 894 rgValGlnIleThrAlaIleGlyAspValLeuGlyProSerIleAsnGlyLeuAlaSerL 914	Qy 874 lnSerThrLeuLysThrLeuSerPheSerPheProProAsnThrValThrGlySerGluA 894	Oy 854 luGlyIleGluLy8SerTyrSerGlnSerIleLeuLeuAspLeuThrAspAsnArgLeuG 874 :::::::::: ::: Db 2823 AAGGAATCAAGCAAGAGCATACCTTCAGCTCACTGTTCTGTGCATCAGATGCTGAGATAT 2882	Qy 844 aValThr	829 ulleProIleThrValThrAla	Qy 809 uValProSerGluAspGlyAlaThrValLeuPheProIleArgProThrHisLeuGlyGl 829 ::: ::	Oy 789 sPheAspIleLeuMetThrSerSerGluIleAsnAlaThrGlyHisGlnGlnThrLeuLe 809	769 r 2541 T	Qy 749 ellePheLeuAsnLeuProTyrSerValIleArgGlyGluGluPheAlaLeuGluIleTh 769 ::: ::::: :::	729 uAspLeuGlyLeuGlyLeuThrThrProValGluLeuGlnAlaPheGlnProPhePh	Qy 709 eG.LuVa.I'InrVa.IProAspSerI.EThrSerTrpVa.IA.aThrGlyPheVallieSerGl 729 ::: ::: :::	: ::: 2304 TTTTCCTGAAACCTGGGTCTGGGATATAGTCACAGTAAACTCCACAGGACTGGCTGAAGT

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                                                            lnPheCysValAsnIleProAlaValArgAsnPheLysValSerAsnThrGlnAspAlaS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 879)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM14090 row: p column: 10
High quality sequence stop: 663.
Location/Qualifiers
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Tissue Procurement: ATCC
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Contact: Robert Strausberg,
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MetLeuThrTrpArgAlaGluGlnGluGlyGlyMetGlnPheTrpValSerSerGluSer
                                                                                                                          AlaLeuIleThrTyrAlaLeuSerSerValGlySerProLysAlaLysGluAlaLeuAsn
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/(clone_lib="NHH_MGC_71"
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                                                     Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                     BQ028040 667 bp mRNA linear I
UI-H-COO-arh-c-08-0-UI.81 NCI_CGAP_Sub9 Homo sapiens
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 667)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                            BQ028040
BQ028040.1 GI:19763319
                              Seq primer: M13 FORWARD POLYA=Yes.
                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             IMAGE: 3106526
                                                                                                                                                                                                                     National Cancer Institute,
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/dev stage="mixed"
/lab host="pH108 (Life Technologies)"
/clone_lib="NCI_CGAP_Sub9"
/clone_lib="NCI_CGAP_Sub9"
/clone_lib="NCI_CGAP_Sub9"
/clone_lib="NCI_CGAP_Sub9"
/note="Vector: pT773-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
carcinoma, Bladder carcinoma, Brain oligodenroga;
NCI_CGAP_Sub9 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are CGTC, AACG, GGGCC,
GGAAG, TAGC, TAGC, ATGG, AGACA, ATCAC. For additional
information. contact: Hento, Soares, bento-soaresmitons adv
TAG_TISSUE=Cervical Adenosquamous Carcinoma
                                                                               information, contact: Bento Soares,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type- ".......9606"
/db_xref="taxon:9606"
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/mol_type="mRNA"
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                                                                                        bento-soares@uiowa.edu
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194 221

US-10-020-095-4 (1-1428) x BQ028040 (1-667) Best Local Similarity: Query Match: Percent Similarity: TyrLysThrSerLeuAsnIleLeuIleLysAspProLysSerAsnLeuIleGlnGlnTrp TyrLysProLysGlnGluValLysPheArgIleValThrLeuPheSerAspPheLysPro ThrArgLeuSerPheGluThrLysArgIleSerValPheIleGlnThrAspLysAlaLeu GAGATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGT GluIleTyrGluLeuArgValThrGlyArgThrGlnAspGluIleLeuPheSerAsnSer 119 PheGluLysGlySerPheLysThrLeuThrLeuProSerLeuProLeuAsnSerAlaAsp AlaGluLeuLeuLysThrAlaSerAsnLeuThrValSerValLeuGluAlaGluGlyVal LeuSerGlnGlnSerAspLeuGlyValIleSerLysThrPheGlnLeuSerSerHisPro TTTGAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGAT 3.71e-109 1117.00 100.00% 100.00% 100.00% 15.20% Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: 667 219 0 0 219 139 546 606 246 199 159 426 486 306 366 99 79

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AL576908.2
                                                                                                                                                                                                                                                                                                                                                                                                         cgi-bin/cluster.cgi?seq=CSODIO81DAO9NP1&cluster=3578.f. C
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation
Faraday Avenue Genoscope sequence ID : CSODIO81DAO9NP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
more information about this cluster, see
http://www.genoscope.cns.fr/
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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                                          TTTGCATCTACTCA-GATACCACT---KTGCTTAAARGYTCTTYTRA-ATTGCAGCCCTA
                                                             PheAlaSerThrGlnAspThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeu 1197
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(bases 1 to 1201)
W.B., Gruber, C.,
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//tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSDORT 6 vector. Library was normalized
a 248 c 224 g 321 t 64 others
                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
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88.84%
88.45%
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
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1495 bp mRNA linear HTC 05-DEC-2002 Mus musculus 3 days neonate thymus cDNA, RIKEN full-length enriched library, clone:A630065N19 product:weakly similar to alpha-2-macroglobulin (fragments) [Limulus polyphemus], full insert
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                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9212, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
prepare mouse tissues.
Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Medicane Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in Disease Wellcome Mechanisms in 
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AAAGGTTCAGGTTCTTAAAAGACGGAGATCTACCGAAAATCAAGAAGTTTTTGATTTA
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US-10-020-095-4 (1-1428) x AK042169 (1-1495)
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URL:http://fantom.gsc.riken.go.jp/
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Please visit our web site for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrThrValAlaLeuLysAlaLeuSerGluPheAlaAlaLeuMetAsnThrGluArgThr 1203
                                                                               AATGTTTCTGCGCATGGCTCGGGATTTGCTATTTGCCAGCTTAATGTTGACTATAACGTG
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LysAlaSerGlySerSerArgArgArgArgSerIleGlnAsnGlnGlnAlaPheAspLeu 1266
                                                                                                                             AsnIleSerAlaAsnGlyPheGlyPheAlaIleCysGlnLeuAsnValValTyrAsnVal
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/protein_id="BAC31190.1"
/brotein_id="BAC31190.1"
/db_xref="G1:26334979"
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VTGPGIPRSIHFRIDSQNLFLLHQEELHALDFITVNVSAHGSGFAICQLNVDYNVKGS
GSSKRRRSTENQEVFPLDVIVNNEDDISHLMLNVCTSHLGSERTGMVLMEVNLLSGFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASSDSIPLSETLKKVEYDNGKLNLYLDSVNESQFCVNIPTVRDYKVSNIRDGSVSVMD
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/clone_Tib="RIKEN full-length enriched
/dev_stage="3 days neonate"
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/db_xref="taxon:10090"
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RESULT 11
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BX386457 Homo sapiens PLACENTA COT 25-NORMALIZED Homo
clone CSODIO81YB18 5-PRIME, mRNA sermann
                                                                                                                                                                                           http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1A1021ZB10QP1&cluster=3578.f. Contact
Feng Liang Email : fllang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1A1021ZB10QP1.
                                                                                                                                                                                                                                                                           Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3578.f more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                          Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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1 (bases 1 to 978)
Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
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/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor v
sites of the pCMVSPORT 6 vector. Library was normalized
                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                Location/Qualifiers
                                                                                                  clone="CSODIO81YB18"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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LysSerAsnG1yG1uPheTrpAspProG1yArgVa1I1eHisSerG1uLeuG1nG1yG1y
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: Noti; Cloned unidirectionally. Primer: Ōligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                           cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtaine from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD
                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Butheria; Primates; Catarrhini; Hom
1 (bases 1 to 638)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UI-H-FG1-bgj-l-22-0-UI.81 NCI CGAP FG1 Hc
UI-H-FG1-bgj-l-22-0-UI 3', mRNA sequence
BU624356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/mol type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clome="UI-H-FG1-Bgj-1-22-0-UI"
/tissue_type="Cell lines"
/dev stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clome lib="NCI CGAP FG1"
/note="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not
                                                                                                                                                                                                                                         ocation/Qualifiers
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NCI CGAP FG1 Homo sapiens
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RESULT 14
BB613975
    DEFINITION
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Best Local Similarity:
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Pred. No.:
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BB613975 648 bp mRNA linear EST BB613975 RIKEN full-length enriched, 0 day neonate head
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                                                                                                                                                                                                            CGTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCATCACTCTTCAGTCATTTTATTTTC
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                                                                                                                                                                                                                                                                                                                                                                                              ACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAG_TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG_SEQ=CGGTCACTC"
139 c 109 g 187 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishkawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramateu, M. and Hayashizaki, Y.
RIKEN Mouse ESTS (Arakawa, T., et al. 2001)
Unpublished
Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus cDNA clone 4832419I01 5',
BB613975
BB613975.1 GI:16454440
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The Institute of Physical and Chemical Research (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashizaki,Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing pipeline with 384 multicapillary sequencer. 10 (11), 1757-1771 (2000)
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Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with uman Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format
/note="Site 1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory
                                                                                              RIKEN. Division of Experimental Animal Research in
                                                                                                                                                                                                                                                                                                                              /tissue_type="head"
/dev_stage="0 day neonate"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                     clone_lib="RIKEN full-length enriched, 0 day neonate
                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="4832419I01"
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This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
Washlu-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 634)
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Fax: 314 286 1810
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                                                                                                      GlyMetAlaLeuMetGluValAsnLeuLeuSerGlyPheMetValProSerGluAlaIle 1314
                                                                                                                                                                                                                                                                         ArgArgSerIleGlnAsnGlnGluAlaPheAspLeuAspValAlaValLysGluAsnLys
                       SerLeuSerGluThrValLysLysValGluTyrAspHisGlyLysLeuAsnLeuTyrLeu 1334
                                                                                                                                                                GATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGT
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//clone lib="Soars NhHMPu S1"
//clone lib="Soars mixed (see below); Vector: pT7T3D-Pac
//note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and se circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 494488-489479."
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/tissue_type="Pooled human melanocyte,
pregnant uterus"
/lab_host="DH10B"
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Result
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ABB82167
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Human r150 protein
Human CD109 K1 pro
Human CD109 K1-H7
Human platelet all
Human r150 protein
Human CD109 K1 var
Human CD109 K1-H7
Human platelet all
Hydrophobic domain
                                                                                                                                                                                                                           Description
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	ABŲ52372	24	1411	'n	1157
	AAB74689	22	248	16.0	1173.5
	AAB43949	21	1285	7	1255
	ABB62921	22	1413	7	1299.5
	ABG28005	22	1542		1315.5
	ABG70020	23	1760	8	1328.5
	ABB63367	22	1760	18.1	1328.5
	ABB99092	23	281	œ	1329.5
	ABG21224	22	1475	œ	1352.5
	ABB09519	23	1479	œ	1376.5
	ABG28006	22	1487	9	1396.5
	ABB71908	22	1425	٥	1406
	ABG61768	23	1492	9	1413.5
	ABG76898	23	1492	19.3	1418.5
	AAR11749	12	1484	9	1425
	AAR11334	12	1474	9.	1428.5
	ABB66669	22	1203	9	1430
	AAU81018	23	1451	9	1437
	AAG63548	22	1508	9	1437.5
	AAU81017	23	1474	19.	1440
	AAU74798	23	1474	19.	1440
	ABP65218	23	1474	19.	1440
	AAB50673	22	1474	19.	1440
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	ABB11581	22	352	21.	1592
	ABB90069	23	336	22.	1628.5
	AAB50677	22	1519	25.	1850
	AAB50676	22	1508	5	1854.5
	AAE32018	24	1445	8	2860.5
	ABB82170	23	1067	4.	5461
	ABB82169	23	1067	4.	5470
	3	24	1399		7068.5
	AAE32014	24	1382	96.4	7081

ALIGNMENTS

AAE32012 standard; Protein; 1428 AA

24-MAR-2003 (first entry)

AAE32012;

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RESULT 1
AAB32012
ID AAB3
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AC AAB3
XX AAB32
XX Huma
DE Huma
XX Huma
XX Huma
XX Huma
XX Homc
CS Homc
CX KW these
FT Key
FT Misc
FT Clea
FT Clea
FT Clea
FT Clea
FT SX
XX WO2(
XX PD 31-(
XX PF 24-1
FR 24-1
FR 24-1
FR 14-1
             24-APR-2001; 2001US-285713P.
14-FEB-2002; 2002US-356163P.
                                                                                                                                                                                                                                                                Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal;
                                                    24-APR-2002; 2002WO-CA00560
                                                                                                        WO200285942-A2
                                                                                                                                              Cleavage-site
                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                       Human r150 protein #1.
                                                                                                                                               /note= "Encoded by TNC"
1404
                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                   /note= "GPI anchor cleavage site"
                                                                                                                                                                        /label= Ser,
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Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for treating cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 94-99; 127pp;
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                                                 ASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEY
                                                                                                                                                                                                                                   SPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWTPKACVIVYY1EDDG
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                                                                                                                                           EIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMN
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                                                                                                                                                                                                                                                                                                                                                                                             KPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQKINY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCS
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Pred. No. 0;
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CD109 K1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
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                                                                                                                                                                                         for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and activation, increased or impaired activation of the coagulation and/or fibrinolytic systems, or impaired activation of the coagulation. These are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, thrombocytopenia, thrombocytopenia, autoimmune disease, organ transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for treating these conditions. The present sequence represents the human
                                                                                                                                                                              or their antisense nucleotide sequence treating these conditions. The present CD109 K1-H7 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to isolated nucleic acid molecules encoding CD109 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-F1, CD109 K15 or their variants. CD109 is a novel member of the alphaz macroglobulin (alphazM)/C3, C4, C5 family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
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  The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion platelet refractoriness or neonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Gova encoded protein.
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N-PSDB; AAD49435.
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14-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal;
                                                                                         Philip
                                                                                                                                                                                                                 24-APR-2002;
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   Novel transforming growth factor (TGF)-beta 1 binding reagent which
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comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for treating cancer -
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Claim 1; Page 103-109; 127pp; English

The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-beta binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein.

1445 AA;

99.6%; 98.7%;

Score Pred.

7318.5; No. 0;

B

24;

Length

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RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWL
                                                                        BIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMV
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                                                                                                                                              ASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEY
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                                                                                                                                                                                                                                                                           ABB82166 standard;
              07-MAR-2001; 2001US-273814P
                                                                                                                                                                                              Human CD109 K1 variant protein.
                                      07-MAR-2002; 2002WO-CA00292
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for treating or detecting a disease or disorder, e.g. conditions associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tlymphocytes and of the complement system, quantitative or qualitative abnormalities of platelet function, increased or impaired platelet aggregation and activation, increased or impaired or increased immune activation and/or fibrinolytic systems, or impaired or increased immune activation. These are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, thrombocytopenia, thrombocythemia, autoimmune diseases, organ transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for
                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated nucleic acid molecules encoding CD10: polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variant; CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, (family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
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DB; ABQ79965.
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SUTHERLAND R
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TVPQSGTFKIEFFILEDSSELQLKAYFLGSKSSMAVHSLFKSFSKTYIQLKTRDENIKVG
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                                                                                                                                                                                                                 MNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSANFSFNDEEMK
                                                                                                                                                                                                                                         MNSKHLNGTI TAKYTYGKPVKGDVTLTFLPLSFWGKKKNI TKTFKI NGSANFS FNDEEMK
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                                                            KPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQKINY
                                                                                                                                        NVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYTTVL
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Matches 1426; Query Match

Conservative

Local Similarity

99.6%; 98.7%;

Score 7317.5; Pred. No. 0; Mismatches

DВ 1; 23;

Indels Length

17; 1445;

Gaps

Sequence

1445

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MELWL 1445
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                                        MELWL 1428
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Claim 21; Fig 3b; 156pp;

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CD109; alpha2 macroglobulin; thioester; cerebroprotective; card immunosuppressive; haemostatic; anticoagulant; thrombolytic; hu cardiovascular; vasotropic; gene therapy; CD109 KI-H7; variant.
                                                                                                                                                                                               New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thromb thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
                                                                                                                                                                                                                                     N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                         Human CD109 K1-H7 variant
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for treating or detecting a disease or disorder, e.g. conditions can be associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes and of the complement system, quantitative or qualitative abnormalities configuration, increased or impaired platelet aggregation and activation, increased or impaired or increased immune activation and/or fibrinolytic systems, or impaired or increased immune activation. These are also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, thrombocytopenia, thrombocythemia, autoimmune diseases, organ transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for treating these conditions. The present sequence represents the human conditions. The present sequence represents the human conditions. The invention relates to isolated nucleic acid molecules encoding CD10 polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1. CD109 K1. CD109 K15 or their variant. CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, Camily of thiosester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid. CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful variants. C3, C4, C5

Sequence 1445 Ā

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                                                                    Query Match
Best Local Simi
Matches 1426;
61
                 61
                                                                              Similarity
                                 ELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNST
ELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNST
                                                                      Conservative
                                                                              99.6%;
                                                                     Score 7317.5;
Pred. No. 0;
1; Mismatches
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RESULT 7 ABB82168

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                         The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion platelet refractoriness or meonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Govb encoded protein.
                                                                                                                                                                                                                                 New isolated oligonucleotide binding to a region of CD109 nucleic acid having a single nucleotide polymorphism that distinguishes a Gova and/or Govb allele, useful for treating blood disorders e.g. alloimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; platelet alloantigen; Gova; Govb; single nucleotide polymorphism; SNP; biallelic; bleeding disorder; post-transfusion purpura; post-transfusion platelet refractoriness; haemostatic; vaccine;
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AAB12127 standard; Protein; 1445

AAB12127;

02-FEB-2001 (first entry)

Hydrophobic domain protein isolated from HT-1080 cells

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Ho Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport; biophylaxis; signal receptor; ion channel; transporter; immunostimulant immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; autoimmune disease; Alzheimer's disease; Parkinson's disease; cancer.

sapiens

WO200029448-A2

25-MAY-2000

17-NOV-1999; 99WO-JP06412.

17-NOV-1998; 22-DEC-1998; 16-MAR-1999; 27-APR-1999; 19-MAY-1999; 99JP-0069811. 99JP-0119299. 99JP-0138169. 98JP-0326255. 98JP-0364315.

(SAGA) (PROT-) SAGAMI CHEM RES PROTEGENE INC.

Kimura H

2000-387753/33. DB: AAA60199, AAA62010.

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Proteins comprising hydrophobic regions, such as secretory and me proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic. secretory and membrane

hemostatic,

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Best Local Similarity
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                                              AERFMEENEGHIVDIHDFSLGSSPHVRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSW
                                                                                                                                                     EIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMN
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VATGFVISEDLGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEV
                              AERFMEENEGHIVDIHDFSLGSSPHVRKHFPETWIWLDTNMGSRIYQEFEVTVPDSITSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta useful for negatively modulating TGF-beta activity, and thus for
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                                                                                                                            Matches 1062;
                                                                                                                                            Best Local Similarity
                                                                                                                                                             Query Match
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytogenia, autoimmune diseases, or organ or bone marrow transplantation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 21; Fig Sa; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human;
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(SUTH/) SUTHERLAND R D.
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ELLKTASNLTVSVLBAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNST
                                                        MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA
                                                                          MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA
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99.9%;
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B82170 B82170 ABB82170 standard; Protein; 1067 AA ABB82170;

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                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated nucleic acid molecules encoding CD10; polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variant; CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, (family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
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                                                                                                                                                                                                                             Sequence
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variant sequence.
             RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWL
                                                                                                                                   MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA
                                  RLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWL 180
                                                                               ELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNST
                                                                                                                   MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKA
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QKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQ
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AAE32018 standard; Protein; 1445 ₿

(first entry)

Human blood cell surface antigen, CD109 #2

Human; GPI-anchored TGF-betal binding protein; glycosylphosphatidyl inositol; transforming gro in; r150 protein; cancer;
growth factor-betal;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human blood cell surface antigen, CD109. CD109 is a variant of r150 sequence.

Note: This sequence is stated to be encoded by human CD109 DNA shown in figure 17 of the specification, but this does not appear to be the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta useful for negatively modulating TGF-beta activity, and thus for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating cancer
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14-FEB-2002; 2002US-356163P.
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                                            KPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQKINY
                                                                                AVMASSAGLSGTLALSSPGPVGILTTVTGSVTGISAAVSTAVPPLGHATIIGPPATTTVL
                                                                                                              NVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYTTVL 360
                                                                                                                                                                                  MNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSANFSFNDBEMK
                                                                                                                                                                                                                                         SQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCS
                  LPSLAPTATVLVTAAAGAGLTLGGAAAAVVITVTGAATTGTTSGSASGAGLMGAVGLIAT
                                                                                                                                                   MASLHLAGTITALTTTGLPVLGAVTLTPLPLSPTGLLLAITLTPLIAGSAAPSPAAGGML
                                                                                                                                                                                                                     SGGSALGVISLTPGLSSHPILGATSIGVGVAAGTTTGSPGVSGTVLPLPGVTLGTPLTCS
                                                                                                                                                                                                                                                                                    ALSPGTLAISVPIGTALALTLPLGGVLPAIVTLPSAPLPTLTSLAILILAPLSALIGGTL 180
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                                                                                                                                                                                                                                                                                                                                                    GLLLTASALTVSVLGAGGVPGLGSPLTLTLPSLPLASAAGITGLAVTGATGAGILPSAST
                                                                                                                                                                                                                                                                                                                                                                                     ELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNST 120
                                                                                                                                                                                                                                                                                                                                                                                                                    MGGPPLLTAAHLLCVCTAALAVAPGPAPLVTAPGIIAPGGAVTIGVGLLGHCPSGVTVLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 2860.5; DB 24; Lengt Pred. No. 3.3e-178; 1; Mismatches 559; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 1445;
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RESULT 15
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AAB50676 standard; Protein; 1508 AA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) a human unc-5HS1 cDNA, useful in yeast two hybrid experiments for identifying unknown human cDNAs which encode proteins that interact
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                 GTITAKYTYGKPVKGDVTLTF-LPLSFW--
                                                                                                                      TFQLSSHPILGDWSIQVQ----VNDQTYYQSFQVSEYVLPKFBVTLQTPLYCSMNSKHLN
                                                                                                                                                               FIQTDRAIYRPASLVRYRAIVVKSDLKPYVGNATIKIFDPSRNLISQTIGVTLDRGVYSG
                                                                                                                                                                                         FIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWLSQQSDLGVISK
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                                                                                                                                                                                                                                                                                                                      VCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVSVL
    ANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDY
                                  VFVDAKYTYGKGVAGKAKVSLELPWHRWHAMVPTIIDENGVKKEEELMVERTVKLNRQGE
                                                                                                ELQLAEETLLGDWFIEVETSNGVQDKS---SFTVDTYVLPKFEVNIKTSSFITIND-DLS
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CTSFSGPGRSGMALMEVNLLSGFMVPSEAISLSETVK----KVEYDHGKLNLYLDSVNE | ::: | | | | | | | : | : | : : : : | | | | | : | : | : : : | |
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                                                  AVSINANGTGVVFAQLSYSY
                                                                              AVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVKENKDDLNHVDLNV
                                                                                                              TSTQDTVMALQALSSYAAVTYSDKHTSQVTILNGKHTHSFDINIRNAIVLQSYQLSSLND
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Listing first 45 summaries
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Sequence 2, Application US/09241606
Patent No. 6472140
GEMERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Kovacs, Dora
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug
TITLE OF INVENTION: Alpha-6765 Applicants and Drug
TITLE OF INVENTION: Alpha-6765 Applicants and Drug
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CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
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TGISRNVSTNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVI 391
                                                  VK--TKVFQLKR-----KEYEMK------LHTEAQIQEEGTVVELTGRQSSEITRTI
                                                                                                       KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT-----TVTESV 331
                                                                                                                                                                                                                                                                 GGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEH-PFTVEEFVLPKFEVQVTVPKIITILE
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                                                                                                                                                          EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ
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29.1%; Pred. No. 5.9e
tive 266; Mismatches
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DLN-HVDLNVCTSFSGPG---RSGMALMEVNILLSGFMVPSEAISL---SETVKKVEYDHG 1328
                                                                                 LPELPGEYSMKVTGEGCVYLQTSLKYNI-
                                                                                                                                                                                                                                                                                               QKPKAPVGHFYEPQAPSAEVENTSYVLLA-YLTAQPAPTSEDLTSATNIVKWITKQQNAQ 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRQGYQRELLYQREDGSFSAFG-NYDPS-GSTWLSAFVLRCFLEADPYIDIDQNVLHRTY 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITAIGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSF 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVS---EELSLKLPPNVVEESARAS
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                                                                                                                                                                                                                                          GGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPSSPSPLAVVQ-------
                                                                                                                                                                                                                                                                                                                                                    VSSESKLSDSWQPR--SLDIEVAAYALLSHFLQFQ---TSEGIP----IMRWLSRQRNSL 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHF 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E----INATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALS-----PTA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSS
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                                                                                                                                                                                        GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LES-----EFSRGISDNYTLALITYALSSVGS-PKAKEALNMLTWRAEQEGGMQFW---
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                                                                                                                                   PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD
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Best Local (
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RESULT 2
US-08-447-411-2
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US-08-447-411-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/447,411
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: DNA ENCODING COBRA C3, NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1651 amin
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1755 S. Jefferson Davis Highway, Suite CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                    A----ELLKTASNLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEIL 115
                                          IQQWLSQQSDLGVISKTFQLSSHPI-----
                                                                                                                                                                                       VHDFPRKQKTLFQSRVDMNQAGSMFVT---PTIKVPAKELNKDSKQNQYVVVKVTGPQVA
                                                                                                                                                                                                                                                                                      MEGMALYLVAALLIGFPGS---SHGALYTLITPAVLRTDTEEQILVEAHGDSTPKSLDIF
                                                                                                                                     FSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNL 175
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                                                                                       LEKVVLLSYQSG--FVFIQTDKGIYTPGSPVRYRVFSV--DHNMHRMDKTVIVE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1651 amino acids
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BREDEHORST, REINHARD
VOGEL, CARL-WILHELM
----FQTPEGIV-----VSSKPVNPSGSIRPYNLPELVSFGTWKAVAKYEHSPEESYT
                                                                                                                                                                                                                                                                                                                                                                                        Conservative 278; Mismatches 649;
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                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 973.5; DB 1; 23.5%; Pred. No. 9.8e-72;
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VAAYALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNTER- 1202
                                              QRPYTTALTAYALA-----AADRLINDDRVLMAASTGRIRW-----EEYNARTHNIE
                                                                                              SDNYTLALITYALSSVGSPKAKEALNMLTWRAEQEGGMQFWVSSESKLSDSWQPRSLDIE
                                                                                                                                                                                                ELQGGNKS---PVTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEFSRG-----I
                                                                                                                                                                                                                                              N--RASSSWLTAYVVKVLAMASNMVKDISHEIICGGVKWLILNRQQPDGVFKENAPVIHG
                                                                                                                                                                                                                                                                                              NYDPSGSTWLSAFVLRCFLEADPYI-DIDQNVLHRTYTWL-KGHQKSNGEFWDPGRVIHS 1036
                                                                                                                                                                                                                                                                                                                                            GEONMITMTPSVIATYYLDATGQWENLGVDRRTEAIKQIMTGYAQQMVYKKADHSYAAFT
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                                                                                                                                               EMLGGTKGAEPEASLTAFIVTALLESRSV-----CKEQINILDSSINKATDYLLKKYEKL
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US-08-793-126-1
; Sequence 1, Application US/08793126
; Patent No. 5849297
; GENERAL INFORMATION:
APPLICANT: Harrison, Richard Alexander
; APPLICANT: Farries, Charles Timothy
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
; NUMBER OF SEQUENCES. 2
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                                                                                                                                                       US-08-793-126-1
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                                                                            Matches
                                                                                                                Query Match
                                                                                                                                                                                                                                              TELEFAX: (617) 526-500
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1663 amino aci
                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 1022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
                                                                                                                                                                   STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 07-FEB CLASSIFICATION: 424
                                                                                            Local Similarity
                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Boston
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GPSLL----LLLLTHLPLALG-SPMYSIITPNILRLESEETMVLEAHDAQGDVPVTVTVH
                                   GPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIR-----PGGNVTIGVELL 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTSYALLALLKMKKFAEVGPVVRWLIDOKYYGGTYGQTQATVMVFQALAEYEIQMPTHQD 1278
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60 State Street
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-FEB-1997
                                                                                                                                                                                                                                                                                                         526-5000
                                                                                            12.7%; Score 931; DB 2; 23.0%; Pred. No. 3.6e-68;
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YQREDGSFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWL-KGHQKSNG 1025
                                                 RLKHLIVTPSGCGEQNMIGMTPTVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLA
                                                                                                    -LASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEK---ALSFMRQGYQRELL
                                                                                                                                                        AV-RTLDPERLGREGVQKE----DIPPADLSDQVPDTESETRILLQGTPVAQMTEDAVDAE
                                                                                                                                                                                                            SILLDLTDNRL--QSTLKTLSFSFPPNTV-----TGSER----VQITAIGDVLGPSING-
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                                                                                   YLDSVNETQ-FCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEV---KLSSCD
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                                                                YLDKVSHSEDDCLAFKVHQYFNVELIQPGAVKVYAYYNLEESCTRFYHPEKEDGKLNK--
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RESULT 4 US-09-132-271-1 Sequence 1, Application US/09132271 Patent No. 6221657 TELEFAX: (617) 526-5000 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: APPLICATION NUMBER: US/08/793
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Baker, Hollie L.
REGISTRATION NUMBER: 31,321
REFERENCE/DOCKET NUMBER: 1022
TELECOMPUNICATION INFORMATION:
TELEPHONE: (617) 526-6000 GENERAL INFORMATION: APPLICANT: Harrison, Richard Alexander
APPLICANT: Farries, Charles Timochy
TITLE OF INVENTION: MODIFIED HUMAN C3 PROTEINS
NUMBER OF SEQUENCES: 2 PRIOR APPLICATION DATA: CURRENT APPLICATION DATA: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy CORRESPONDENCE ADDRESS: MEDIUM TYPE: Floppy disk-COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, FILING DATE: COUNTRY: UN CITY: Boston STATE: MA STREET: CLASSIFICATION: APPLICATION NUMBER: ADDRESSEE: 60 State Street United States of HALE AND DORR LLP US/08/793,126 US/09/132,271 102286.377 America Version #1.30

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Matches 376
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TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
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                                                                                           APPLICANT: FAITIES, Timothy C.
APPLICANT: Harries, Timothy C.
APPLICANT: Harries, Richard A.
TITLE OF INVENTION: Down-Regulation Resistant C3
FILE REFERENCE: 4-30443/A/MU/PCT
CURRENT APPLICATION NUMBER: US/09/142,334
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: PCT/GB97/00603
EARLIER FILING DATE: 1997-03-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 22
TENEVERI. 1663
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ORGANISM: Homo
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Best Local Similarity 23.0 Matches 376; Conservative
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                                                                                                          QQTLLVPSEDGATVLFPIRP--THLGEIPITVTALSPTASDAVTQMILVKAEGIEKSYSQ
                                                                                                                                                       DFFIDLRLPYSVVRNEQVEIRAVLYNY-RONQELKVRVELLHNPAFCSLATTKR----RH
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                                                                                                                                                                                                                                                                                 ------LDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTTTPVELQAFQ 746
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286; Mismatches 615; Indels
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APPLICANT: Rother, Russell P.
APPLICANT: Springhorn, Jeremy P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Squinto, Stephen P.
APPLICANT: Thomas C.
APPLICANT: Wilkins, James A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: OF INFLAMMATORY DISEASES NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                            ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.4Mb
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APPLICANT:
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                                                                                                                                                                  ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park
CITY: New Haven
    COMPUTER: Macintosh Cetris
OPERATING SYSTEM: System 7
SOFTWARE: WordPerfect 3.0
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Mueller, Eileen
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AUTHORS: Wets
TITLE: Comple
Patent NO. 6355245
TITLE: Comple
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Best Local S
Matches 379
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1676 Amino Acids
TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: HOMO DEFINITION:
PUBLICATION INFORMATION:
AUTHORS: Haviland, J.C.
AUTHORS: Haviland, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (203)776-1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
DESCRIPTION: Pro-C5 Polytpeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: AL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tch 12.5%; Score 921; DB 4; Length 1676;
al Similarity 24.0%; Pred. No. 2.5e-67;
379; Conservative 297; Mismatches 621; Indels 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVISAPKIFRVGASENIVIQVYGYTEAFDATISIKSYPDKKFSYSSGHVHLSSENKFQNS
                                                                                                                                                                                                                                        KYTYGKPV-KGDVTLTFLPLSFWGKKKNI-----TKTFKINGSANFSFNDEEM
                                                                                                                                                                                                                                                                                                             LGDWSIQVQVNDQ----TYYQSFQVSBYVLPKFEVTLQTPLYCSM---NSKHLNGTITA
                                                                                                                                                                                                                                                                                                                                                                                                                                           AILTIQPKQLPGGQNPVSYVY-LEVVSKH-----FSKSKRMPITYDNGFLFIHTDKPVYT 136
                                         PLFLKPGIPYPIKVQV-----KDSLDQLVGGVPVILNAQTIDVNQETSDLDPSKSVTRV
                                                                                                                                                                                                   RYFYNKVVTEADVYITF-----GIREDLKDDQKEMMQTAMQNTMLINGIAQVTFDSE--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFKTLTLPSLP--LNSADEIYELRVTGRTQDEILFSNSTRLSFETKRISVFIQTDKALYK 141
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      MEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLK 471
                                                                                TTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVI-----TVTQRNYTEYWSGSNSGNQK 411
                                                                                                                                                            KNVMDSSNGLSEYL -- DLSSPGPVEILTTVTESVTGISRNVS-TNVFFKQHDYIIEFFDY
                                                                                                                                                                                                                                                                                 YGMWTIKAKYKEDFSTTGTAY - - PEVKEYVLPHFSVSIE - PEYNFIGYKNFKNFEITIKA
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                                                           GNSDYKRIVACASYK-PSREESSSGSSHAVMDISLPTGISANEEDLKALVEGVDQLFTDY 1453
                                                                                                                                                                              AVVOPMAVN----ISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQ-EAFDLDVAVKENK
                                                                                                                                                                                                                                                          NSLGGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPSSPS------PL
                                                                                                                                                                                                                                                                                               NPPIYRFWKDNLOHKDSSVPNTGTARM--VETTAYALLTSLNLKDINYVNPVIKWLSEEQ
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                                                                                                  DDLNHVDLNVCTSFSGPGR-----
                                                                                                                                       EVL----LNDDLIVSTGFGSGLATVHVTTVVHKTSTSEEVCSFYLKIDTQDIEASHYRGY 1394
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-GKLMLYLDSVNETQF-CVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEV 1382
                                                                                                SGMALMEVNLLSGFMVPSEAI-SLSETVKKVEYDH
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1274 1338 1218 1278

QY 243 SKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSANFSFNDEE 298 :::: : : : : : : : : : : :	Qy 188 VISKTFQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCSMN 242	Qy 128 RISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWLSQQSDLG 187	Qy 68 NLTVSVLEAEGYFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSFETK 127	OY 18 AALAVAPGPRELUTAPGIIRPGGNUTIGUELL-EHCPSQUTUKAELLKTAS 67	Query Match 12.2%; Score 894; DB 2; Length 1642; Best Local Similarity 22.3%; Pred. No. 4.4e-65; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56;	PE	DEDNESS:	; SEQUENCE CHARACTERISTICS; ; LENGTH: 1642 amino acids : TYPE: amino acid	; TELEFAX: 703-413-2220 ; INFORMATION FOR SEQ ID NO: 2:	E/DOCKET NUMBE ICATION INFORM	; ATTORNEY/AGENT INFORMATION: ; NAME: OBLON, NORWAN F. REGISTRATION NUMBER: 24.618	APPLICATION NUMBER: US/08/662,227 APPLICATION NUMBER: US/08/662,227 FILING DATE: 14-UN-1996	SOFTWARE: Patentin Release #1.0, Version #1.30	COMPUTER: IBM PC compatible COMPUTER: PC-DOS/MS-DOS	Y: USA 22202	ARLINGTON VA	ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY	PONDENCE ADDRESS:	9 C	KOCK, MICHAE	; GENERAL INFORMATION: ; APPLICANT: VOGEL, CARL-WILHELM · ADDITCANT. BEFIELDEST BEINLORST	·	227-2		1512SNIKIQKVCEGAA	Qy 1383 KLSSCDLCSDVQGCRPCEDGA 1403	Db 1454 QIKDGHVILQLNSIPSSDFLCVRFRIFELFEVGFLSPATFTVYEYHRPDKQCTMFYST 1511
28	Db !	Q B 4	S B &	; B &	? B &	Db	Qy	Db	g Q	Oy Db	Db .	? ₽	Q	Db .		Q	ממ	γQ	ממ	Q	מם	ρ	dd 4g	?	Db ?	 О	Дb
1189 NALSEMALMKIEK LNIQVIVISESSESELT	EEYNAHTHNIEGTSYALLALLKMKKFDQTGPIVRWLTDQNFYGETYGQTQATVMAF		1069 ORSTHELESESRGISDNYTLALITTVALSSVGSPKAKFALLNMITWRAEOEGGMOFWVSSE 1128		OS GPSINGLASLIKMPYGGGEQNMINFAFNIILDITIKKKQUIDNIKEKALSFYKQ	915 VVPEGVQKSIVTIVKLDPRAKGVGGTQLEVIKARKLDDRVPDTEIETKIIIQGDPVAQII 974		857C\$ASTKGQRYRQQPPIKALSSRAVPFVIVPLEQGLHDVEIKASVQEALWSDGVRKKLK 914	793 LMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALSPTASDAVTQMIL 850	733 LGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDI 792 :	747 SRSDFPKSWLWLTKDLTEEPNSQGISSKTMSFYLRDSITTWVVLAVSFTPTKG 799		650GHIVDIHDF 678	627 ALTTSTNLNTKQRSAAKCPQPANRRRRSSVLLLDSNASKAAEFQDQDLRKCCEDVMHENP 686	ISQAKIWDTIĖKSDFGCTAĠSGQNNLGVFE	579 SVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGL 638	516 PSFRFVAYYQVGNNEIVADSVWVDVKDTCMGTLVVKGDNLIQMPGAAMKIKL 567	527 PKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRI 578	456 PGDNLPVNFNVKGNANSLKQIKYFTYLILNKGKIFKVGRQPRRDGQNLVTMNLHITPDLI 515	479 VGSPFELVVSGNKRLKELSYMVVSRGQLVAVGKQNSTMFSLTPENSWT 526	399 ILNIPUNAQSLPITVRTNHGDLPRERQATKSMTAIAYQTQGGSGNYLHVAITSTEIK 455	419 NYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIK 4	353 YFKPGMPYELTVYVTNPDGSPAAHVPVVSEAFHSMGTTLSDGTAKL 398		FRSRFDNLNELVGHTLYASVTVMTESGSDMVVTEOSGIHIVASPYQIHFTKTPK	299 MKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDYTT 358	241 -ENFHVSITARYLYGEEVEG-VAFVLFGVKIDDAKKSIPDSLTRIPIIDGDGKATLKRDT 298

Query Match 12.2%; Score 894; DB 4; Length 1642; Best Local Similarity 22.5%; Pred. No. 4.4e-65; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 276; Gaps 56; Matches 361; Conservative 295; Mismatches 672; Indels 295; Mismatches 672; Indels 295; Mismatches 295; Mismatches 295; Mismatches 295; Mismatches 295; M	HARACTERISTICS: 1642 amino acid mino acid ness: single : linear YPE: protein	ATTORNEY AGENT INFORMATION: NAME: OBLON, NORMAN F. REGISTRATION NUMBER: 24,618 REFERENCE/DOCKET NUMBER: 1126-0107-0X TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000 TELEPHONE: 703-413-2200 INFORMATION TO NO. 2:	OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/017,947 FILING DATE: CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION UMBER: US 08/662,227	INGTON INGTON USA DE: FORDABLE FORDABLE FORDE: FLOORDABLE	SELL SELL SELL SELL SELL SELL SELL SELL	
Q b Q b Q	5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	O	p & p &	D	B & B & B &	
905 GPSINGLASLIRMPYGCGEQMMINFARMIYILDYLTKKKOLTONLKEKALSEYRQ 959	TO SELECTION OF THE CONTROL OF THE C	SUGSSHYRKHYEETWING	9 WVLTDANL-TKD	527 PKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYMSKVKAEPSEKVSLRI 578	359 VLKPSLNITATVKVTKADENCLILEEKKNINVITTVYCKNYTEYWSGSNSGNOKMEAVQK. 418	

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RESULT 9
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                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,747
FILING DATE: 07-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-101-0
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 113-3000
                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1, 1, CITY: Arlington Virginia
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APPLICANT: BREDEHORST, REINHARD
APPLICANT: VOGEL, CARL-WILHELM
                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palana
                                                           TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT.
ADDRESSEE: P.C.
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1755 S. Jefferson Davis Highway, Suite
1642 amino acids
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
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Best Local Similarity
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                     857 -- CSASTKGQRYRQQFPIKALSSRAVPFVIVPLEQGLHDVEIKASVQEALWSDGVRKKLK
                                                                                                                                                                                                                                                                                                                                                                                          639 WVLTDANL-TKD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  128 RISVFIQTDKALYKPKQEVKFRIVTLFSDFKPYKTSLNILIKDPKSNLIQQWLSQQSDLG 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 NLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSFETK 127
                                                                                                                                     LGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTGYYLGMFMNSFAVFQECGL
                                                           LMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLG--EIPITVTALSPTASDAVTQMIL
                                                                                                                                                                                 S-----RSDFPKSWLWLTKDLTEEPNSQGISSKTMSFYLRDSITTWVVLAVSFTPTKG
                                                                                                                                                                                                                            SLGSSPHVRKHFPETWIWL-----DTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLG
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                                                                                                       I-CVAEPYEIRVMKVFFIDLQMPYSVVKNEQVEIRAILHNYVNEDIYVRVELLYNPAF--
                                                                                                                                                                                                                                                                      MGYTCEKRAKYIQEGDACKAAFLECCRYIKGVRDENQRESELFLARDDNEDGFIADSDII
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RESULT 10
US-08-662-227-35
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; GENERAL INFORMATION:
APPLICANT: VOGEL, C.
APPLICANT: BREDEHORS
APPLICANT: KOCK, MIC
APPLICANT: FRITZING:
APPLICANT: FRITZING:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -08-001
Sequence 35, Appring No. 5922320
                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                              ADDRESSEE: OBLOW, ...
ADDRESSEE: P.C.
ADDRESSEE: P.C.
CORRET: 1755 S. JEFFERSON DAVIS HIGHWAY
                           APPLICATION NUMBER: US/0 FILING DATE: 14-JUN-1996
                                                                                                                                                                                                      COUNTRY: U
ZIP: 22202
      CLASSIFICATION:
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FRITZINGER, DAVID
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BREDEHORST, REINHORST
                                                                                                                                                                                                                                                                                                                                     OBLON, SPIVAK, MCCLELLAND, MAIER
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 1126
REFERENCE/DOCKET NUMBER: 1126
TELECOMMUNICATION INFORMATION:
TELEPHANE: 703-413-3000
TELEPHAX: 703-413-2220
TELEPHAX: 703-413-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                   NSWTPKACVIVYYIEDDGEIISDVLKIPVQ-----LVFK--NKIKLYWSKVKAEPSEKV
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IHDFSLGSSPHVRKHFPETWIWL-----DTNMGYRIYQEFEVTVPDSITSWVATGFVIS 728
                                           HENPMGYTCEKRAKYIQEGDACKAAFLECCRYIKGVRDENQRESELFLARDDNEDGFIAD
                                                                                                                               DAGLALTTSTNLNTKQRSAAKCPQPANRRRRSSVLLLDSNASKAAEFQDQDLRKCCEDVM
                                                                                                                                                                             ECGLWVLTDANL-TKD-----
                                                                                                                                                                                                                                                              SLRISVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTGYYLGMFMNSFAVFQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GN-ENFHVSITARYLYGEEVEG-VAFVLFGVKIDDAKKSIPDSLTRIPIIDGDGKATLKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNI----TKTFKINGSANFSFND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LGVISKTFQLSSHPILGDWSI--QVQVNDQTYYQSFQVSEYVLPKFEVTLQTP---LYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --FLFIQTDKGIYTPGSPVLYRVFSM--DHHTSKMNKTVIVEFQTPEGILVS---SNSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSFETK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AALLIGFPGSSHGALYTLITPAVLRTDTEEQILVEAHGDSTPKQLDIFVHDFPRKQKTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                             IKVGS--PFELVVSGN----KRLKELSYMVVSRGQLVAVGKQNS-----TM-FSLTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLILNIPLNAQ---SLPITVRTNHGDLPRERQATKSMTAIAYQTQGGSGNYLHVAITSTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQ 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DTFRSRFPNLNELVGHTLYAS-----VTVMTESGSDMVVTEQSGIHIVASPYQIHFTKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNFF~WPYNLPDLVSLGTWRIVAKYEHSPENYTAYFDVRKYVLPSFEVRLQPSEKFFYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1648 amino acids
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                                                                                                                                                                                                                      VGLVAVDKAVYVLNDKYKISQAKIWDTIEKSDFGCTAGSGQNNLGVFE
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                                                                                     -YIDGVYD-NAEYAERFM--EENE-GHIVD
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RESULT 11
US-09-017-947-35
                                                                                                                                                                                                                                                                                              Sequence 35, Application US/09017947
Patent No. 6303754
GENERAL INFORMATION:
STREET: 1/J
CITY: ARLINGTON
                                                                                                                                                     APPLICANT: KOCK, MICHAEL
APPLICANT: FRITZINGER, DAVID
TITLE OF INVENTION: RECOMBINANT PROCVF
NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                    CORRESPONDENCE ADDRESS
                                                             ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C. STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1366 KICTRYLGEVDSTMTIIDISMLTGFLPDAEDLTRLSKGVDRYISRYEVDNNMAQKVAVII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1486 IGNVCRCAGETCSSLNHQERIDVPLQIEKACETNVDYVYKTKLLRIEE 1533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1254 VMAFQALAEYEIQMPTHKDLNLDITIELPDREVPIRYRINYENALLARTVETKLNQDITV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        847 QMILVKAEGIEKSYSQSILLDLTDNRLQST-----LKTLSFSFPPNTVTGSERVQITAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NVCTSFSGPGRSGMALMEVNLLSGFMVPSEAIS----LSETVKKVEYDHGKLN-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TASGDGKATMTILTFYNAQL----QEKANVCNK--FHLNVSVE--NIHLNAMGAKGALML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- EEYNAHTHNIEGTSYALLALLKNKKFDQTGPIVRWLTDQNFYGETYGQTQAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D---VQESIHFLESEFSRGISDNYTLALITYALSSVGSPKAKEALNMLTWRAEQEGGMQFW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIVTGYAQQMVYKKADHSYAAFTN--RASSSWLTAYVVKVFAMAAKMVAGISHEIICGGV 1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCF-LEADPYIDIDQNVLHRTY 1014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVALKALSEFAALMNTER-TNIQVTVTGPSSPSPL-----AVVQP---MAVNI 1228
                                                                                                                                                                                                                                                    VOGEL, CARL-WILHELM
BREDEHORST, REINHORS
                                                                                                                                                                                                                                                    REINHORST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----HSSVIFIFCFKLLYFME 1425
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 703-413-2220 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 703-413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
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                                                                                                                                                                                                                                                                                                 351 PKYFKPGMPYELTVYVTNPDGSPA-----AHVPVVSEAF-----HSMGTTLSDGTA 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 MNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGKKKNI----TKTFKINGSANFSFND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 LGVISKTFQLSSHPILGDWSI--QVQVNDQTYYQSFQVSEYVLPKFEVTLQTP---LYCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 RISVFIQTDXALYKPKQEVKFRIVTLFSDFKPYKTSLNILI--KDPKSNLIQQWLSQQSD 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 QTRVDMNPAGGMLVT---PTIEIPAKEVSTDSRQNQYVVVQVTGPQVRLEKVVLLSYQSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 NLTVSVLEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSFETK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AALLIGFPGSSHGALYTLITPAVLRTDTEEQILVEAHGDSTPKQLDIFVHDFPRKQKTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 AALAV-----APGPRFLVTAPGIIRPGGNVTIGVELL-EHCPSQVTVKA----ELLKTAS
                                                             NSWTPKACVIVYYIEDDGEIISDVLKIPVQ-----LVFK--NKIKLYWSKVKAEPSEKV
              LIPSPR--FVAYYQVGNNEIVADSVWVDVKDTCMGTLVVKGDNLIQMPGAAMKIKLEGDF
                                                                                                                                                                                                   KLILNIPLNAQ---SLPITVRTNHGDLPRERQATKSMTAIAYQTQGGSGNYLHVAITSTE
                                                                                                                                                                                                                                                                                                                                             TTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITVTQRNYTEYWSGSNSGNQKMEAVQ 416
                                                                                                                                                                                                                                                                                                                                                                                           DTFRSRFPNLNELVGHTLYAS-----VTVMTESGSDMVVTEQSGIHIVASPYQIHFTKT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                          EEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGISRNVSTNVFFKQHDYIIEFFDY 356
                                                                                                                                                       IKVGS--PFELVVSGN----KRLKELSYMVVSRGQLVAVGKQNS-----TM-FSLTPE
                                                                                                                                                                                                                                                KINYTVPQSGTFKIEFPILEDSSELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --FLFIQTDKGIYTPGSPVLYRVFSM--DHHTSKMNKTVIVEFQTPEGILVS---SNSVD
                                                                                                         I KPGDNLPVNFNVKGNANSLKQIKYFTYLILNKGKIFKVGRQPRRDGQNLVTMNLHITPD
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RESULT 12
US-08-447-411-76
; Sequence 76, Application US/08447411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSSESKLSDSWQPRSLDIEVAAYALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSSIKKATNYLLKKYEK-LQRPYTTALTAYALA-----AADQLNDDRVLMAASTGRDHW 1201
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                                                                                                                        IGNVCRCAGETCSSLNHQERIDVPLQIEKACETNVDYVYKTKLLRIEE
                                                                                                                                                                                                                YLNKVSHSEDECLHPKILKHFEVGFIQPGSVKVYSYYNLDEKCTKFYHPDKGTGLLNKIC
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 10.5%; Score 768.5; DB 1; Best Local Similarity 24.4%; Pred. No. 9.7e-55; Matches 301; Conservative 208; Mismatches 477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5773243
GENERAL INFORMATION:
APPLICANT: FRITZINGER, DAVID C.
APPLICANT: BREDEHORST, REINHARD
APPLICANT: VÖGEL, CARL-WILHELM
TITLE OF INVENTION: DNA ENCODING
NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/043,
PILLING DATE: 07-APR-1993
ATTORNEY/ACENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/447,411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1333 amino acids
TYPE: amino acid
TOPOLOGY: linear
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    AGSGQNNLGVFEDAGLALTTSTNLNTKQRSAAKCPQPANRRRRSSVLLLDSNASKAAQFQ 353
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Y: U.S.A.
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GENERAL A.:

APPLICANT: BREDEHORS:

APPLICANT: KOCK, MICHAEL

APPLICANT: FRITZINGER, DAVID

TITLE OF INVENTION: RECOMBINANT PROCVF

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND,
                                                                                                                                                                                                                                                                                                                                   RESULT 13
US-08-662-227-34
                                                                                                                                                                                                                                                                                       Sequence 34, Application US/08662227 Patent No. 5922320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PNTVTGSERVQITAIGDVLGPSING--LASLIRMPYGCGEQNMINF-APNI--YILDYLT 940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LAVVQPMAVN----ISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQBAFDLDVA 1269
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                                                                                                                                                                                                                                                                                                                                                                                                                           EKCTKIYHPDEATGLLNKICVGNVCRCAEETCS
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Best Local Similarity
Matches 301; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,227
FILLING DATE: 14-JUN-1996
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1333 amino acidd
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION
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NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1755 S. CITY: ARLINGTON
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                                                                ADKDIYVRVELLYSPAFCSASTESQ----RYREQLPIKALSSRAVSFVIVPLEQGLHDVE 578
                                                                                                     LKDATEVKVIIEKSDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLG--EIP
                                                                                                                                                                                        VATGFVISEDLGLGLTTT------PVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNY
                                                                                                                                                                                                                                           ARSDFEDDLFGEGNITSRSDFPESWLWLMEQLSEHPNSKGISSKIVPFY---LRDSITTW
                                                                                                                                                                                                                                                                                     ---DIHDFSLGSSPHV-RKHFPETWIWL-----DINMGYRIYQEFEVTVPDSITSW
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                                                                                                                                                        ELLAVGLSPTKGICVAEPYEITVMKDFFIDLQLPYSVVKNEQVKIRAVLYNY
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 34,
COUNTRY: USA
ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UMMBER: US/09/017,947
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: RE NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                             STREET: 1755 S.
CITY: ARLINGTON
                                                                                                                                                                                                                                                           ADDRESSEE:
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BREDEHORST, REINHORST
KOCK, MICHAEL
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                                                                                                                                                                                                                                                                             OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-0107-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
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KKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTWLSAFVLRCF-LEA 999
                                     DTEIETKITIQGDFVAQTIENSIDGSKLNHLIITPFGCGEQNMIRMTAPVIATYYLDTTQ 698
                                                                                                                                                                                                                                                                                                                                                          ARSDFEDDLFGEGNITSRSDFPESWLWLMEQLSEHPNSKGISSKIVPFY---LRDSITTW
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                                                                            PNTVTGSERVQITAIGDVLGPSING--LASLIRMPYGCGEQNMINF-APNI--YILDYLT
                                                                                                                 VTASVQGELMSDGVKKKLKVVPEGEWKSIVTIIELDPHTKGIGGTQVELVKANKLNDRVP
                                                                                                                                                      ITVTALSPTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQST-----LKTLSFSFP
                                                                                                                                                                                               ADKDIYVRVELLYSPAFCSASTESQ----RYREQLPIKALSSRAVSFVIVPLEQGLHDVE
                                                                                                                                                                                                                                    LKDATEVKVIIEKSDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLG--EIP
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Conservative 208;
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Pred. No. 6.6e-54;
DB; Mismatches 477; Indels 247;
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RESULT 15
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Patent No. 5322838
TELEFAX: (202) 833-871
TELEX: 248636 SSK
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Silberstein, David S.
APPLICANT: Minkoff, Marjorie
TITLE OF INVENTION: INHIB, A Factor Which Inhibits
TITLE OF INVENTION: Cytokine-Activated Leukocytes
NUMBER OF SEQUENCES: 3
                                                                                                                                                    FILING UALL.
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FOX, Samuel L.
NAME: TOX NIMBER: 30,353
                                                                                               REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 06
TELECHMUNICATION INFORMATION:
TELECHONE: (202) 466-0800
                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19911016
                                                                                                                                                                                                                                                                                                                           ZIP: 20036-2678
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                        SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K----VEYDH-----GKLNLYLDSVNETQ-FÇVNIFAVRNFKVSNTQDASVSIVDYYEPR 137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VENVQLNLKEAKGAKGALKĹKICTRYLGEVDSTMTIIDVSMLTGFVPDTEDLTRLSKGVD 109:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V-----KENKDDLNHVDLNVCTSFSGPGRSGMALMEVNLLSGFMVPSEAIS-LSETVK 1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENALLAQTVETKLNEDFTVSASGDGKATMTILTVYNAQL----REDANVCNK--FHLDVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LAVVQPMAVN----ISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVA 1269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QWLIDQQYYGGTYGQTQATVMMFQALAEYEIQMPTHKDLNLDITIELPDREVPIRYRINY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sterne, Kessler, Goldstein & Fox 1225 Connecticut Avenue, N.W.
    645 amino acids
                                                                                (202) 833-8716
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                                                                                                                                                                                                                                                                      US/07/779,172A
                                                                                                                                           0627.1270001
                                                                                                                                                                                                                                                                                                              Version
                                                                                                                                                                                                                                                                                                              #1.25
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; TOPOLOGY: both
; MOLECULE TYPE: peptide
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Best Local Similarity
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                               VHELELYNTGYYLGMFMNSFAVFQECGL 638
WDVVEKADIGCTPGSGKDYAGVFSDAGL
                                                                                                                                                                                                                                                                                GVAKLSINTHPSQK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNLTVSV-LEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQ--DEILFSNSTRLS
                                                                                                    KNKIKLYWSKVKAE----PSEKVSLRISVTQPDSIVGIVAVDKSVNLMNASNDITMENV
                                                                                                                                     QVREPGQDLVVLPLSITTDFIPSFRLVAYYTVIGASGQREVVADSVWVDVKDSCVGSLVV
                                                                                                                                                                         ----QNSTMFSLTPENSWTPKACVIVYY----IEDDGEIISDVLKIPVQ-----LVF
                                                                                                                                                                                                            YSTVGNSNNYLHLSVLTTELRPGETLNVNFLLRMDRAHEAKIRYYTYLIMNKGRLLKAGR
                                                                                                                                                                                                                                             SLFKSPSKTYIQLKTRDENIKVGSPFELVV-----SGNKRLKELSYMVVSRGQLVAVGK
                                                                                                                                                                                                                                                                                                               YTEYWSGSNSGNOKMEAVOKINYTVPQSGTFKIEFPILEDSSELOLKAYFLGSKSSMAVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMYSIITPNILRLESEETMVLEAHDAQGDVPVTVTVHDFPGKKLVLSSEKTVLTPATNHM
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                                                                   QSEDROPVPGQQMTLK1EGDHGARVV-LVAVDKGVFVLNKKNKLTQSKI
                                                                                                                                                                                                                                                                                --PLSITVRTKKQELSEAEQ-----ATRTMQALP
622
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Search completed: January 15, 2004, 18:15:19
Job time : 33 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

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16: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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   2 US-10-108-260A-3396

2 US-10-369-493-5314

2 US-10-369-493-5313

2 US-10-292-081A-15

4 US-10-052-817-2

US-09-873-403-5

US-09-873-403-5

US-10-292-081A-10

US-10-292-081A-12

US-10-292-081A-13

12 US-10-292-081A-13

12 US-10-292-081A-38

12 US-10-292-081A-38

12 US-09-756-247-4

12 US-09-756-247-23

12 US-09-756-247-23

12 US-09-756-247-25

12 US-09-756-247-25

12 US-09-756-247-25

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12 US-09-756-247-25

12 US-09-756-247-25

12 US-09-756-247-25

12 US-09-756-247-25
Sequence 3396, Ap
Sequence 5311, Ap
Sequence 5313, Appl
Sequence 15, Appl
Sequence 2, Appli
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 38, Appl
Sequence 38, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 26, Appli
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3396
LENGTH: 665
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US-10-108-260A-3396
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Best Local Sim
Matches 657;
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al Similarity 100.0%;
657; Conservative 0;
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0; Mismatches 0;
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/03-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
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Best Local
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                          ELQLAEETLLGDWFIEVETSNGVQDKS---SFTVDTYVLPKFEVNIKTSSFITIND-DLS
                                                                                                               FIQTDRAIYRPASLVRYRAIVVKSDLKPYVGNATIKIFDPSRNLISQTIGVTLDRGVYSG
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  AVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVKENKDDLNHVDLNV
                                               TSTQDTVMALQALSSYAAVTYSDKHTSQVTILNGKHTHSFDINIRNAIVLQSYQLSSLND
                                                                                         ASTODTTVALKALSEFAALMNTERTNIQVTV-TGPSSPS-----PLAVVQPM-----
                                                                                                                                         SAOKKVEKLKESRAYMFOARPVDIETTSYAVLSYLAONOTSESLSIIRWLVSORNELGGF
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: DLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
FRIOR APPLICATION NUMBER: US 60/360,039
FRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 5313
LENGTH: 1519
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 25.2%; Score 1850; DB 12; Local Similarity 31.6%; Pred. No. 9.9e-143; tes 477; Conservative 290; Mismatches 563;
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                                                          KCG--EDCWP 1483
                                                                                                LCSDVQGCRP 1398
                                                                                                                                       KMNVYFNPLGGRPVCLSLYSDVTYQVADQKPANFRLVDYYDPEEQLKMTYAAKQTRSLQE 1475
                                                                                                                                                                         KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCD
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                                                                                                                                                                                                                                                                                                                                                                                  LVSQRNELGGFTSTQDTVMALQALSSYAAVTYSDKHTSQVTILNGKHTHSFDINIRNAIV
                                                                                                                                                                                                                                                                                                                                                                                                                     LSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTNIQVTV-TGPSSPS-----PLAV 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -AEQEGGMQFWVSSE--SKLSDS----WQPRSLDIEVAAYALLSHFLQFQTSEGIPIMRW 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL-----ENGMENGKAVTYLEKHLDEVSGNAYTMAVVAYALQLAKSKQAGKAFENLKKHK 1185
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Publication No.
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APPLICANT: Gonul Velicelebi
APPLICANT: Xin Wang
APPLICANT: Randolph E. Tanzi
APPLICANT: Lars Bertram
APPLICANT: Aleister J. Saunders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Aleister J. Saunders
TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGIC
FILE REFERENCE: 37481-3323
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ORGANISM: Homo sapiens
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                                                              EIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLM- 599
                                                                                                                            LKELS--YMVVSRGQLVAVG-----KQNST----MFSLTPENSWTPKACVIVYYIEDDG
                                                                                                                                                                                                                                                       TVTQRNYTEYWSGSNSGNQKMEAVQ-KINYT--VPQSGTFKIEFP------ILEDS 438
                                                                                                                                                                                                                                                                                                                                                     VK--TKVFQLKR-----KEYEMK------LHTEAQIQEEGTVVELTGRQSSEITRTI
                                DVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAA-PQSVCALRAVDQSVLLMK 608
                                                                                                                                                                                           SELQLKAYFLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGS----PFELVVSGNK--R
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                                                                                             LKKLSFYYLIMAKGGIVRTGTHGLLVKQEDMKGHFSISIPVKSDIAPVARLLIYAVLPTG
                                                                                                                                                             EEAHHTAY --
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No. US20030162202A1
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   - NDITMENVVHELELYNTGY - YLGMFMNS - - - - FA
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                                                                                                EPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSN
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                                                KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNS
                                                                                                                                                     DLN-HVDLNVCTSFSGPG---RSGMALMEVNLLSGFMVPSEAISL---SETVKKVEYDHG
                                                                                                                                                                                                        LPELPGEYSMKVTGEGCVYLQTSLKYNI------LPEKEEFPFALGVQTLPQTCD
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US-10-052-817-2
; Sequence 2, Application US/10052817
; Publication No. US20020114792A1
; GENERAL INFORMATION:
; APPLICANT: Tanzi, Rudolph E.
; APPLICANT: Kovaccs, Dora
; APPLICANT: Saunders, Aleister J.
; TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and Drug Screening Methods
; TITLE OF INVENTION: Alzheimer's Disease
; FILE REFERENCE: 0609.4460005
; CURRENT APPLICATION NUMBER: US/10/052,817
; CURRENT FILING DATE: 2002-01-23
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SEQ ID NO 2
LENGTH: 1474
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Best Local Similarity
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PRIOR TILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 60/093,297
PRIOR FILING DATE: 1998-07-17
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FILING DATE: 1999-02-02
APPLICATION NUMBER: 09/148,503
FILING DATE: 1998-09-04
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RESULT 6
US-09-873-403-5
VS-09-873-403-5

| Sequence 5, Application US/09873403
| Patent NO. US20020028207A1
| GENERAL INFORMATION:
| APPLICANT: STIVESTAVA, Pramod K
| TITLE OF INVENTION: COMPLEXES OF ALPHA (2) MACROGLOBULIN AND ANTIGENIC
| TITLE OF INVENTION: MOLECULES FOR IMMUNOTHERAPY
| FILE REFERENCE: 8449-178
| CURRENT APPLICATION NUMBER: US/09/873,403
| CURRENT FILING DATE: 2001-06-04
| PRIOR APPLICATION NUMBER: 09/625,139
| PRIOR APPLICATION NUMBER: 09/625,139
| PRIOR APPLICATION NUMBER: 09/625,139
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                                      PEHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVS---EELSLKLPPNVVEESARAS
                                                                                                                                                                                                                                                                                      GSSPH---VRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSWVATGFVISEDLGLGLTT 737
                                                                                                                                           E----INATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTALS-----PTA 841
                                                                                                                                                                                                                TPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSS
                                                                                                                                                                                                                                                                                                                       FLEDMGLKAFTNSKIRKPKMCPQLQQYEMHGPEGLRVGFYESDVMGRGHARLVHVEE---
                                                                                                                                                                                                                                                                                                                                                                                                                             ASNDITMENVVHEL-ELYNTGY------YLGMFMNS------FA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMN 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKELS--YMVVSRGQLVAVG-----KONST----MFSLTPENSWTPKACVIVYYIEDDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGVISKTFQLSSHPILGDWSIQVQVND--QTYYQSFQVSEYVLPKFEVTLQTPLYCSMNS
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   ITAIGDVLGPSINGLASLIRMPYGCGEQNMINFAPNIYILDYLTKKKQLTDNLKEKALSF 956
                                                                                                                                                                             T-ASLRAFQPFFVELTMPYSVIRGEAFTLKATVLNYLPKCIRVSVQLEASPAFLAVPVEK 84:
                                                                                                                                                                                                                                                                                                                                                           VFQECGLWVLTDANLTKDYIDGVYDNAE-----YAERFMEENEGHIVDIHDFSL
                                                                                                                                                                                                                                                                                                                                                                                          PDAELSASSVYNLLPEKDLTGFPGPLNDQDDEDCINRHNVYINGITYTPVSSTNEKDMYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ 303
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                                                                     --SDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQ 896
                                                                                                                                                                                                                                                   PHTETVRKYFPETWIWDLVVVNSAGVAEVGVTVPDTITEWKAGAFCLSEDAGLGISS
                                                                                                           -----TVSWAVTPKSLGNVNFTVSAEALESQELCGTEVPSV 890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --LVFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGGTLLG 489
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
LENGTH: 1474
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                                                                                                                                                                                                       Query Match
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APPLICANT:
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-10-292-081A-10
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TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLOG
FILE REFERENCE: 37481-3323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
PRIOR APPLICATION NUMBER: 60/337434
PRIOR APPLICATION NUMBER: 60/337434
PRIOR FILING DATE: 2001-11-09
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                                                                                                                                                                               Local Similarity
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                                                                                                                      12 LLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTIGVELLEHCPSQVTVKAELLKTASNLTV
                                        -SVLEAEG-VFEKGSFKTLTLPSLPLNSADE---IYELRVTGRTQDEILFSNSTRLSFET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKPKAPVGHFYEPQAPSAEVEMTSYVLLA-YLTAQPAPTSEDLTSATNIVKWITKQQNAQ 1245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLN-HVDLNVCTSFSGPG---RSGMALMEVNLLSGFMVPSEAISL---SETVKKVEYDHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSSESKLSDSWQPR--SLDIEVAAYALLSHFLQFQ---TSEGIP----IMRWLSRQRNSL
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                                                                                LLVLLPTDASVSGKPQYMVLVPSLLHT-ETTEKGCVLLSYLNETVTVSASLESVRGNRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LESAWKTAQEGDHG-SHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVKKDNSVHWERP 1186
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                                                                                                                                                               19.6%; Score 1440; DB 12; ilarity 29.1%; Pred. No. 6.7e-109; Conservative 266; Mismatches 551;
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                                                               IWLSQRQKDNGCFRSSGSLLNNAIKGGVEDEVTLSAYITIALLEIPLTVTHPVVRNALFC
                                                                                                                               TWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHF
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/292,081A CURRENT FILING DATE: 2002-11-08 PRIOR APPLICATION NUMBER: 60/337434 PRIOR FILING DATE: 2001-11-09 NUMBER OF SEQ ID NOS: 15
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APPLICANT: Aleister J. Saunders
TITLE OF INVENTION: SINGLE NUCLEOTIDE
FILE REFERENCE: 37481-3323
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APPLICANT: Gomul Velicelebi
APPLICANT: xin Wang
APPLICANT: Randolph E. Tanzi
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                                                                                            244 KHLNGTITAKYTYGKPVKGDVTLTFLPL---
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                        EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ 303
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                                                                                                                                                               GGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEH-PFTVEEFVLPKFEVQVTVPKIITILE
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----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD 1275
                                                                                                                         GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS
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Matches
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PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 13
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TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS
FILE REFERENCE: 37481-3323
CURRENT APPLICATION NUMBER: US/10/292,081A
CURRENT FILING DATE: 2002-11-08
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                                                                                                                                               VK--TKVFQLKR-----KEYEMK------LHTEAQIQEEGTVVELTGRQSSEITRTI
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                                                KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNS 1380
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                                                                                                            EPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSN
                                                                                                                                                          DLN-HVDLNVCTSFSGPG---RSGMALMEVNLLSGFMVPSEAISL---SETVKKVEYDHG 1328
                                                                                                                                                                                                                                                                 ----PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD
                                                                                                                                                                                                                                                                                                                  GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS
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US-10-331-496A-38
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US-10-331-496A-38
; Sequence 38, Application US/10331496A
; Publication No. US20030228305A1
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PRIOR FILLING DATE: 2002-01-02
PRIOR APPLICATION NUMBER: US 60/351,885
PRIOR FILLING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 60/360,066
PRIOR APPLICATION NUMBER: US 60/362,004
PRIOR APPLICATION NUMBER: US 60/362,004
PRIOR APPLICATION NUMBER: US 60/362,004
PRIOR APPLICATION NUMBER: US 60/366,869
PRIOR APPLICATION NUMBER: US 60/366,869
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SEQ ID NO 38
LENGTH: 1474
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APPLICANT: HILLAN, KENNETH
APPLICANT: PHILLIPS, HEIDI
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PRIOR APPLICATION NUMBER: US 60/368,679
PRIOR FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/404,809
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CURRENT APPLICATION NUMBER: US/10/331,496A
CURRENT FILING DATE: 2002-12-30
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PRIOR APPLICATION NUMBER: US 60/366,284
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VK--TKVFQLKR-----KEYEMK-----LHTEAQIQEEGTVVELTGRQSSEITRTI
                                                                                                                                                                                                                                                               LGVISKTFQLSSHPILGDWSIQVQVND--QTYYQSFQVSEYVLPKFEVTLQTPLYCSMNS
                                                                                                                                                                                                                                                                                                                                                KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT-----TVTESV 331
                                                                                                       EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ
                                                                                                                                                                                                              GGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEH-PFTVEEFVLPKFEVQVTVPKIITILE
                                                                                                                                                                                                                                                                                                                EDSLVFVQTDKSIYKPGQTVKFRVVSMDENFHPLNELIPLVYIQDPKGNRIAQWQSFQLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLVLLPTDASVSGKPQYMVLVPSLLHT-ETTEKGCVLLSYLNETVTVSASLESVRGNRSL
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PHILLIPS, HEIDI
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DLN-HVDLNVCTSFSGPG---RSGMALMEVNILLSGFMVPSEAISL---SETVKKVEYDHG 1328
                                                                                 LPELPGEYSMKVTGEGCVYLQTSLKYNI--
                                                                                                                                                                                                                                                                                                     QKPKAPVGHFYEPQAPSAEVEMTSYVLLA-YLTAQPAPTSEDLTSATNIVKWITKQQNAQ 1245
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T-ASLRAPQPFFVELTMPYSVIRGEAFTLKATVLNYLPKCIRVSVQLEASPAFLAVPVEK 841
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                                                                                                                                                                                                                                            GGFASTQDTTVALKALSEFAALMNTERTNIQVTVTGPSSPSPLAVVQ------
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                                                                                                                                                                                            GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS 1304
                                                                                                                                                                                                                                                                                                                                                          VSSESKLSDSWQPR--SLDIEVAAYALLSHFLQFQ---TSEGIP----IMRWLSRQRNSL 1175
                                                                                                                                                                                                                                                                                                                                                                                                                  LESAWKTAQEGDHG-SHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVKKDNSVHWERP 1186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHF 1074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LES----EFSRGISDNYTLALITYALSSVGS-PKAKEALNMLTWRAEQEGGMQFW---
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                                                                                                                                       PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD
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정 음 성 음

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APPLICANT: Liu, Chenghous
APPLICANT: Yeung, George
APPLICANT: Yeung, George
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS REL
TITLE OF INVENTION: AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-31CIP
CURRENT APPLICATION NUMBER: US/09/756,247
CURRENT APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/644,711
PRIOR FILING DATE: 2000-01-06
PRIOR APPLICATION NUMBER: 09/664,711
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 09/660,875
PRIOR PILING DATE: 09/496,914
PRIOR FILING DATE: 2000-02-03
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 1508
TYPE: PRT
ORGANISM: Homo sapiens
US-09-756-247-4
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US-09-756-247-4
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Publication No. US20030180722A1
GENERAL INFORMATION:
APPLICANT: Godbole, Shubhada D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 422;
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                                                                                                                                                                                                                                                                                                                                                                             74 LEAEGVFEKGSFKTLTLPSLPLNSADEIYELRVTGRTQDEILFSNSTRLSFETKRISVFI 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 LAVAPG-----PRFLVTAPGIIR-PGGNVTIGVELLEHCPSQVTVKAELLKTASNLTVSV
TDKTGCFSAPVDMATFDLIGYAYSHQINIVATVVBEGTGVEANATQNIYISPQMGSMTFE
                                                                                                                                                              QTDKPLYTPGQQVYFRIVTMDSNFVPVNDKYSMVELQDPNSNRIAQWLEVVPEQGIVDLS
                                                                                                                                                                                                                                                                                                                                        LEYSGLKKRHLHCISFLVPPPAGGTEEVATIRVSG-VGNNISFEEKKKVLIQRQGNGTFV 124
                                                                                  RYTYGKPMLGAVQVSVC----QKAN---
                                                                                                                         KYTYGKPVKGDVTLTFLPLSFWGKKKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEY
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                                         LD----LSSP-----
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Tang, Y. Tom
Liu, Chenghua
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Arterburn, Matthew
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Mize, Nancy K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.6%; Score 1437.5; DB 12; Length 1508; ilarity 27.1%; Pred. No. 1.1e-108; Conservative 274; Mismatches 552; Indels 307; Gaps
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                                       --GPVEILTTVTESVTGISRNVSTNVFFKOHDYIIEFF
                                                                                       ----TYWYREVEREQLPDKCRNLSGQ 285
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1211 -GPSSPSFLAVVQPMAVNISANGFGFAICQLNVVYNVKASGSSRRI	1159 SEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTNIQVTVT :: : : : : : : :	1107 ALMMLTWRAEQEGGMQFWVSSESKLSDSW-QPRSLDIEVAAYALLSHFLQFQ	1048 LTAYIVTSLLGYRKYQPNIDVQESIHFLESEFSRGISDNYTLALITYALSSVGSPKAKE- : : : : : : : : : :	988 LSAFVLRCFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVT : : : :	928 NFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDGSFSAFGNYDPSGSTW	889 VTGSERVQITAIG	838SPTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSF	787 SDKFDILMTSSEINATGHQQTLLVPSEDGATVLFPIRPTHLGEIPITVTAL	727 ISEDLGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEK :	667 ENEGHIVDIHDFSLGSSPHVRKHFPETWIWLDTNMGYRIVQEFEVTVPDSITSWVATG	627MNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEYA ; ; ; ; ; ; ; ; ; ; ;	608 ENVYHELELYNTGYYLGMF	548 KIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMNASNDITM	498 YMVVSRGQLVAVGKQNSTMPSLTPENSWTPKACVIVYYIEDDGBIISDVL :::	447 FLGSKSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKRLK : ::	398YTEYWSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKA	O TO DESCRIPTION OF THE PROPERTY AND INDUSTRIAL PROPERTY OF THE PROPERTY OF TH
SGSSR P	ERTNIQVTVT 1210 	ALLSHFLQFQT 1158 : 	ITYALSSVGSPKAKE- 1106	<pre>RVIHSELQGGNKSPVT 1047 :: : :: : vLLHTAMKGGVDDEVS 1116</pre>	3SFSAFGNYDPSGSTW 987 : : : SYSAFGERDGNGNTW 1056	ASLIRMPYGCGEQNMI 927 :: : DGLVQMPSGCGEQNMV 996	DLTDNRLQSTLKTLSFSFPPNT 888 : :: : : SLLCPKGKVASESVSLELPVDI 936	PITVTAL 837 :: FTISTKILDSNEPCG 881	?NYLKDATEVKVIIEK 786 : ?NYLKDCIRVQTDLAK 827	/TVPDSITSWVATGFV 726 : /TVPDAITEWKAMSFC 768	/AERFME 666 : /STAMGGGGHPEAFES 716	626 PQPLIDPMPQGHSSQR 657	DKSVNLMNASNDITM 607	[VYYIEDDGEIISDVL 547 	SGNKRLKELS 497 :: : DPADASPDQEI-SFS 490	-FPILEDSSELQLKAY 446 :: :: VPRYYQNAYLHLRPF 445	KNHLVFLVIYGTNGTFNQTLVTDNNGLAP 400

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US-09-756-247-23
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CURRENT APPLICATION NUMBER: US/09/756,247
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-217
PRIOR PRILING DATE: 2000-03-31
PRIOR PRILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/684,711
PRIOR APPLICATION NUMBER: 09/684,711
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/50,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR PILING DATE: 2000-02-03
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO ALPHA-2-MACROGLOBULIN-LIKE
TITLE OF INVENTION: AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.5%; Score 1433; DB 12;
Local Similarity 29.0%; Pred. No. 2.5e-108;
Les 450; Conservative 265; Mismatches 551;
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                                         231
                                                                                                                                                186 LGVISKTFQLSSHPILGDWSIQVQVND--QTYYQSFQVSEYVLPKFEVTLQTPLYCSMNS
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  277 KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT-----TVTESV 331
                                                                                244 KHLNGTITAKYTYGKPVKGDVTLTFLPL-----
                                                                                                                                                                                                             112 EDSLVFVQTDKSIYKÞGQTVKFRVVSMDENFHPLNELIPLVYÍQDPKGNRÍAQWQSFQLE
                                                                                                                                                                                                                                                                                         61 FTDLEAENDVLHCVAF-----AVPKSSSNEEVMFLTVQVKGPTQE---FKKRTTVMVKN 111
                                                                                                                                                                                                                                                                                                                                   72 -SVLEAEG-VFEKGSFKTLTLPSLPLNSADE---IYELRVTGRTQDEILFSNSTRLSFET 126
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Deng, Cenhua
Goodrich, Ryle
Arterburn, Matthew C
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                                       EEMNVSVCGLYTYGKPVPGHVTVSICRKYSDASDCHGEDSQAFCEKFSGQLNSHGCFYQQ
                                                                                                                          GGLKQFSFPLSSEPFQGSYKVVVQKKSGGRTEH-PFTVEEFVLPKFEVQVTVPKIITILE
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Tang, Y. Tom
Liu, Chenghua
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                                                                                ---SFWGK 276
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                                                                                                                                                                                                QKPKAPVGHFYEPQAPSAEVEMTSYVLLA-YLTAQPAPTSEDLTSATNIVKWITKQQNAQ 1232
                                                                                                                                                                                                                                   VSSESKLSDSWQPR--SLDIEVAAYALLSHFLQFQ---TSEGIP----IMRWLSRQRNSL 1175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTGYQRQLNYKHYDGSYSTFGERYGRNQGNTWLTAFYLKTFAQARAYIFIDEAHITQAL 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRQGYQRELLYQREDGSFSAFG-NYDPS-GSTWLSAFVLRCFLEADPYIDIDQNVLHRTY 1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEHGRKDTVIKPLLVEPEGLEKETTFNSLLCPSGGEVS---EELSLKLPPNVVEESARAS
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                                                                                                                                                                                                                                                                                                                                                                                                                             VSVLGDILGSAMQNTQNLLQMPYGCGEQNMVLFAPNIYVLDYLNETQQLTPEVKSKAIGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLEDMGLKAFTNSKIRKPKMCPQLQQYEMHGPEGLRVGFYESDVMGRGHARLVHVEE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VFQECGLWVLTDANLTKDYIDGVYDNAE-----YAERFMEENEGHIVDIHDFSL 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDAELSASSVYNLLPEKDLTGFPGPLNDQDDEDCINRHNVYINGITYTPVSSTNEKDMYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASNDITMENVVHEL-ELYNTGY------YLGMFMNS------FA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMV 600
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                                                                                                                                          GGFASTODTTVALKALSEFAALMNTERTNIQVTVTGPSSPSPLAVVQ-----
                                                                                                                                                                                                                                                                                                             LESAWKTAQEGDHG-SHVYTKALLAYAFALAGNQDKRKEVLKSLNEEAVKKDNSVHWERP
                                                                                                                                                                                                                                                                                                                                                 LES----EFSRGISDNYTLALITYALSSVGS-PKAKEALNMLTWRAEQEGGMQFW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHF 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITAIGDVLGPSINGLASLIRMPYGCGEQNMINPAPNIYILDYLTKKKQLTDNLKEKALSF 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E----INATGHOQTLLVPSEDGATVLFPIRPTHLGEIPITVTALS-----PTA 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVIGDSAKYDVENCLANKVDLSFSPSQSLPASHAHLRVTAA-PQSVCALRAVDQSVLLMK 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TVTQRNYTEYWSGSNSGNQKMEAVQ-KINYT--VPQSGTFKIEFP-----ILEDS 438
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                                                                                     GGFSSTQDTVVALHALSKYGAATFT-RTGKAAQVTIQSSGTFSSKFQVDNNNRLLLQQVS 1291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----SDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSFSFPPNTVTGSERVQ 896
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-PMAVNISANGFGFAICQLNVVYNVKASGSSRRRRSIQNQEAFDLDVAVK---ENKD 1275
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APPLICANT: Zhou, Ping
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Yeung, George
APPLICANT: Yeung, George
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: METHODS AND MATERIALS REI
TITLE OF INVENTION: AND POLYNUCLEOTIDES
FILE REFERENCE: HYS-31CIP
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR APPLICATION NUMBER: 09/649,217
PRIOR APPLICATION NUMBER: 09/64,711
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/560,875
PRIOR APPLICATION NUMBER: 09/496,914
PRIOR APPLICATION NUMBER: 09/496,914
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US-09-756-247-25
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Best Local (
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                                        VTLTFLPLSFWGKKKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLD----LSSP-
                                                                                                           WSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGD
VQVSVC-----QKAN------TYWYREVEREQLPDKCRNLSGQTDKTGCFSAPV
                                                                                    YT--VAVAEGKTFGTFSVEEYVLPKFKVEVVEPKELSTVQESFLVKICCRYTYGKPMLGA
                                                                                                                                                                     QVYFRIVTMDSNFVPVNDKYSMVELQDPNSNRIAQWLEVVPEQGIVDLSFQLAPEAMLGT 178
                                                                                                                                                                                                       EVKFRIVTLFSDFKPYKTSLNIL-IKDPKSNLIQQWLSQQSDLGVISKTFQLSSHPILGD
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Mize, Nancy K
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Goodrich, Ryle
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                                                                                                                                                                                                                                                                                                                                          ADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDPGRVIHSELQGGNKSPVTLTAYIVTSLLG 1058
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KOHNAYGGFSSTODTVVALQALAKYATTAYMPSEEINLVVKSTENFQRTFNIQSVNRLVF 1289
                                              RQRNSLGGFASTQDTTVALKALSEFA--ALMNTERTNIQVTVT------GPSSPSPLAV 1220
                                                                                             SGESIYWSQKPTPSSNASPWSEPAAVDVELTAYALLAQLTKPSLTQKEIAKATSIVAWLA
                                                                                                                                               EGGMQFWVSSESKLSDS--W-QPRSLDIEVAAYALLSH----FLQFQTSEGIPIMRWLS
                                                                                                                                                                                                MGKDVDDPMVSQGLRCLKNS-ATSTTNLYTQALLAYIFSLAGEMDIRNILLKQLDQQAII 1169
                                                                                                                                                                                                                                                                                                   AQKFIFIDPKNIQDALKWMAGNQLPSGCYANVGNLLHTAMKGGVDDEVSLTAYVTAALLE
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APPLICANT: Kenneth David Becker

APPLICANT: Kenneth David Becker

APPLICANT: Gonul Velicelebi

APPLICANT: Almang

APPLICANT: Xin Wang

APPLICANT: Lars Bertram

APPLICANT: Lars Bertram

APPLICANT: Aleister J. Saunders

TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS AND MUTATIONS ON ALPHA-2-MACROGLO

FILE REFERENCE: 37481-3323

CURRENT APPLICATION NUMBER: US/10/292,081A

CURRENT APPLICATION NUMBER: 60/337434

PRIOR APPLICATION NUMBER: 60/337434

PRIOR APPLICATION NUMBER: 60/337434

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FASESEQ for Windows Version 4.0
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Matches
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TYPE: PRT
ORGANISM: Homo
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nes 458; Conserv
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FI-RGNEANYY--SNATTDEHGLVQFSINTTNVMGTSLTVRVNYKDRSPCYGYQWVSEEH
                                   TVTQRNYTEYWSGSNSGNQKMEAVQ-KINYT--VPQSGTFKIEFP-----ILEDS 438
                                                                                                                                                                                                             KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILT-----TVTESV 331
                                                                                                                                                                                                                                                                                                                                             GGLKOFSFPLSSEPFOGSYKVVVOKKSGGRTEH-PFTVEEFVLPKFEVQVTVPKIITILE
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                                                                                  TKLS-FVKVDSHFRQG---IPFFG---
                                                                                                                          TGISRNVSTNVFFKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVI 391
                                                                                                                                                                   VK--TKVFQLKR-----KEYEMK------LHTEAQIQEEGTVVELTGRQSSEITRTI
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                                                                                  -QVRLVDGKGVPIP----NKVI
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HVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYYE-----TGDLQLLSTM 1464
                                                                                                                                                                                                                                   LPELPGEYSMKVTGEGCVYLQTSLKYNI------LPEKEEFPFALGVQTLPQTCD
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                                                    KLNLYLDSVNETQFCVNIPAVRNFKVSNTQDASVSIVDYYEPRRQAVRSYNSEVKLSSCD 1388
                                                                                                              EPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSN
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                                                                                                                                                                         DLN-HVDLNVCTSFSGPG---RSGMALMEVNLLSGFMVPSEAISL---SETVKKVEYDHG 1328
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PRIOR FILING DATE: 2000-10-17
PRIOR PPLICATION NUMBER: 60/241,243
PRIOR APPLICATION NUMBER: 60/242,152
PRIOR APPLICATION NUMBER: 60/242,152
PRIOR PILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/242,482
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,611
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,611
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SEQ ID NO 10
LENGTH: 149
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Publication No. US20030212256A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R
APPLICANT: Gerlach, Valerie
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Best Local :
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CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: 60/241,040
PRIOR PILING DATE: 2000-10-17
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                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: 60/242,881
PRIOR FILING DATE: 2000-10-24
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APPLICANT: Gorman, Linda
TITLE OF INVENTION: Proteins and Nucleic Acids
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Spytek, Kimberly A
Spytek, Kimberly A
Gangolli, Esha A
LALSPAIAEELPNYLVTLPARLNFP----SVQKVCLDLSPGYSDVKFTVTLETKDKTQKL
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Taupier Jr, Raymond
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Peyman, John A
Stone, David J
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Malyankar, Muriel M
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838SPTASDAVTQMILVKAEGIEKSYSQSILLDLTDNRLQSTLKTLSF 882	
779 EVKVIIEKSDKFDILMTSSEINATGHQOTLLVPSEDGATVLFPIRPTHLGEIPITVTAL- 837 :	
719 SWVATGFVISEDLGLGLTTTPVELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDAT 778	
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627 MNSFAVFQECGLWVLTDANLTKDYIDGVYDNAEYA 661	
600 NASNDITMENVVHELELYNTGYYLGMF626	
540 GEIISDVLKIPVQLVFKNKIKLYWSKVKAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLM 599 ::: :: :	
ELSYMVVSRGQLVAVGKQN :: : ::: SFSYYLIGKGSLVMEGQKHLNSK	
TYIQLKT	
394 TORNFTEYWSGSNSGNQKMEAVQKINYTVPQSGTFKIEFPILEDS 438	
344 FKQHDYIIEFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVITV 393	
302 VMDSSNGLSEYLDLSSPGPVEILTTYTESVTGISRNVSTNVF 343	
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193 FQLSSHPILGDWSIQVQVNDQTYYQSFQVSEYVLPKFEVTLQTPLYCSM 241 :	
134 QTDKALYKÞKQEVKFRIVTLFSDFKÞYKTSLNIL-IKDÞKSNLIQQWLSQQSDLGVISKT 192 	
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Search completed: January 15, 2004, 18:19:33 Job time: 51 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14, Ap 14, Ap 14, Ap 68, Ap 76, Ap 9774, 10198,	327, 322, 1803	Sequence 80, Appl Sequence 60, Appl Sequence 9, Appli Sequence 2, Appli Sequence 83, Appli Sequence 81, Appl	3, 1, 4, 1, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4, 4,	Description Sequence 1174, Ap Sequence 1, Appli

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US-09-220-132-94	US-09-308-003-6	US-09-077-674-4	US-09-077-675A-4	US-09-236-949-1	US-08-322-760A-1	US-08-542-003-1	US-09-601-198-52	US-09-311-352B-3	US-09-601-198-41	US-09-813-133A-3	US-09-017-947-1	US-08-662-227-1	US-08-447-411-44	US-08-559-896B-1	US-09-252-991A-9867	US-09-620-312D-154	US-09-434-408-3
Sequence 94, Appl	Sequence 6, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 52, Appl	Sequence 3, Appli	Sequence 41, Appl	Sequence 3, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 44, Appl	Sequence 1, Appli	Sequence 9867, Ap	Sequence 154, App	Sequence 3, Appli

ALIGNMENTS

RESULT 1 US-09-016-434-1174

Sequence 1174, Application US/09016434 Patent No. 6500938

GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Sellhamer
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION

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; LIBRARY: GENBA; CLONE: 9177869
US-09-016-434-1174
                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
FILING DATE:
Query Match
Best Local Similarity
                                                                                                                                                                                                                      TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                     LENGTH: 4079 base pairs
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3174 PORTER DRIVE
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                                                                                                                                          linear
                                                                                                                                                               single
  2.6%;
                                                                                                                                                                                                                                                                                                                             PA-0002 US
  Pred. No. 3.1e-21;
                  Length 4079;
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Gaps

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APPLICANT: Tanzi, Rudolph E.
APPLICANT: Kovacs, Dora
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alpha-2-Macroglobulin Therapies and
TITLE OF INVENTION: Alzheimer's Disease
FILE REFERENCE: 0609.1465003
CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-241-606-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09241606 Patent No. 6472140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: sig_peptide
LOCATION: (44)..(112)
                                                 NAME/KEY: CDS
LOCATION: (44)..(4468)
                               FEATURE:
                                                                                                                                                                                                                      ENGTH: 4577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2829 ACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGTTACCAGAG 2888
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                                                                                                                                                                                                                                                                                                                                                                                              and Drug Screening
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| Sequence 14, Application US/08232463 |
| Patent NO. 5670367 |
| GENERAL INFORMATION: RECOMBLINGER, F. APPLICANT: FALKMER, F. G. |
| APPLICANT: FALKMER, F. G. |
| APPLICANT: FALKMER, F. G. |
| TITLE OF INVENTION: RECOMBLINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
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; LOCATION: (113)..(4468)
US-09-241-606-1
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Best Local Similarity 50.2%;
Matches 303; Conservative
SIALLY
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                        STREET: 1800 Dia
CITY: Alexandria
                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCAGAATATGGTCCTCTTTGCTCCTAACATCTATGTACTGGATTATCTAAATGAAACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATCAGCCTAACATTGATGTGCAAGAGTCTATCCATTTTTTGGAGTCTGAATTCAGTAG 3242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGTAGAAGATGAAGTGACCCTCTCCCCCCTATATCACCATCCCCCTTCTGGAGATTCCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGGACAATGGCTGTTTCAGGAGCTCTGGGTCACTGCTCAACAATGCCATAAAGGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACCAGGCAACACCTGGCTCACAGCCTTTGTTCTGAAGACTTTTGCCCCAAGCTCGAGC
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1800 Diagonal Road,
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                                                                                                                                                                                Suite
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3024 2828 2964

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GENERAL INFORMATION:
APPLICANT: Webb, Donna J.
APPLICANT: Gonias, Steven L.
TITLE OF INVENTION: Transforming Growth Factor-beta Binding
FILE REFERENCE: 00370-02
CURRENT APPLICATION NUMBER: US/09/311,352B
CURRENT FILING DATE: 1999-05-13
                                                                                                                Sequence 1, Application US/09311352B Patent No. 6329500
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Best Local Similarity
Matches 18; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
FILING DATE:
APPLICATION NUMBER: E
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CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                               1449
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                                                                                                                                                                                                               RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRATCGCAAGCTCC 1055
                                                                                                                                                                                                                                                                                TGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTAGTATCCAG 1508
                                                                                                                                                                                                                                                                                                                                            TAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGATCGCCTTT
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In Release #1.0, Version #1.25
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RESULT 5
US-08-447-411-1
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 339
; TYPE: DNA
; ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-311-352B-1
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Best Local Similarity
                                                                     TELEPHONE: (703) 413-300
TELEPAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773243man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 1126-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/043,747
FILING DATE: 07-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: DNA ENCODING COBRA C3, CVF1, AND CVF2 NUMBER OF SEQUENCES: 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1755 S.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                       STRANDEDNESS:
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                                                           LENGTH:
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    Application US/08447411
    5773243

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                   i: 5211 base pairs
   nucleic acid
DEDNESS: unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U.S.A.
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unknown
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                                                                                                                                                                                                                                                                                                                                                                                           Version
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RESULT 7
US-09-241-606-3
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US-09-241-606-5
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LOCATION: (1)..(333)
OTHER INFORMATION: A
US-09-241-606-5
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                                                        Sequence 3, Application US/09241606
Patent No. 6472140
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Tanzi, Rudolph E.
APPLICANT: Kovacs, Dora
APPLICANT: Saunders, Aleister J.
APPLICANT: Saunders, Aleister J.
TITLE OF INVENTION: Alzhea-2-Macroglobulin Therapies
TITLE OF INVENTION: Alzheimer's Disease
TILE REFERENCE: 0609.4460003
CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILLNG DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5, Application US/09241606 Patent No. 6472140
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Best Local Similarity
Matches 113; Conserv
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                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 5
APPLICANT: Tanzi, Rudolph E. APPLICANT: Kovacs, Dora APPLICANT: Saunders, Aleister J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 333
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION:
                                                                                                                                                                                                                                                                                                        3481 GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT 3540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3376 TCATCAGAGTCCAAACTTTCTGACTCCTGGCAGCCACGCTCCCTGGATATTGAAGTTGCA
                                                                                                                                                                                                                                3541 ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCC 3588
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                                                                                                                                                                                                                                                                                                                                                 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCTACTCAGGATACCACT
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                                                                                                                                                                                                                                                                       GCAACCAACATCGTGAAGTGGATCACGAAGCAGCAGAATGCCCAGGGCGGTTTCTCCTCC
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                                                                                                                                                                                             ACCCAGGACACAGTGGTGGCTCTCCATGCTCTGTCCAAATATGGAGCC 126
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Pred. No. 0.012;
0; Mismatches 111; Indels
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CURRENT APPLICATION NUMBER: US/09/241,606
CURRENT FILING DATE: 1999-02-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Ver. SEQ ID NO 11
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Best Local Similarity
Matches 68; Conserv
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CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
EARLIER FILING DATE: 1998-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228N
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ORGANISM: Homo :
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Margarit, S. M. APPLICANT: Bor-Sogi, Dafna
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LOCATION: (1)..(750)
OTHER INFORMATION: A /LRP Binding Domain
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                                                            2791 CAAATTTTTGAAAAATTAAATAATGCTACAGGTGAACACTTAAAAATTATAAGTAAACCC 2850
982 ACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACTAATGTGTTCTTCAAGCAACAT
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                                                                                               GGACTITCTGAATACCTGGATCTATCTTCCCCTGGACCAGTAGAAATTTTAACCACAGTG
                                                                                                                                           AGGAAGAAAAATATCCATTAACTGTAGACACTTTGAATACAATGAAGAAGAAGAAATCCTCG 2790
                                                                                                                                                                              GGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGATGAAAAATGTAATGGATTCTTCAAAT 921
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Pred. No. 0.016;
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TITLE OF INVENTION:
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APPLICANT: Bult et
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Sequence 1, Application US/08916421B
Patent No. 6503729
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LOCATION: (10398)..(10398)
COTHER INFORMATION: n equals
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LOCATION: (98343)
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OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (713652)...(713652)
OTHER INFORMATION: n equals a,
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                                 LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals
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LOCATION: (779676)..(779676)
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NAME/KEY: misc_feat
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LOCATION: (7416
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NAME/KEY: misc_feature LOCATION: (231980)..(231980) OTHER INFORMATION: n equals ç ņ ú ç ö ö õ 얁 ω ιQ Q g

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                                                                                   APPLICANT: Cassell, Gail H
APPLICANT: Chen, Ellson y
APPLICANT: Class, Jennife
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl
APPLICANT: Lefkowitz, Ell
                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                              Sequence 80, Application US/09601198 Patent No. 6531583
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Best Local
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APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREALYTICUM
TITLE OF INVENTION: UREALYTICUM
FILE REFERENCE: URB-13452/22
CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
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LOCATION: (1569020)..(1569020)
OTHER INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
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LOCATION: (1664854)..(1664855)
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LOCATION: (1637998)..(1637998)
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OTHER INFORMATION: n equals a,
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LOCATION: (1603734)..(1603734)
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LOCATION: (1602912)..(1602912)
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LOCATION: (1470091)..(1470091)
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LOCATION: (1349491)..(1349491)
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LOCATION: (1349473)..(1349473)
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LOCATION: (1313224)..(1313224)
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LOCATION: (1119881)..(1119881)
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LOCATION: (1310988)..(1310988)
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RESULT 11
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; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-80
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                                                                              ; ORGANISM: Ureaplasma urealyticum 
US-09-601-198-60
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APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
                                                                                                                                                         SOFTWARE: Pa
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PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 60, Application US/09601198 Patent No. 6531583
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Matches 175; Conserv
Query Match 0.8
Best Local Similarity 48.8
Matches 112; Conservative
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                                                                                                                                                                                                                                                        TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA TITLE OF INVENTION: UREALYTICUM FILE REFERENCE: UAB-13452/22 CURRENT APPLICATION NUMBER: US/09/601,198 CURRENT FILING DATE: 2000-12-08
                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 181
                                                                                                                     TYPE: DNA
                                                                                                                                       ENGTH:
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Score 39.4; DB Pred. No. 2.9; 0; Mismatches
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Pred. No. 0.4;
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                                       DB 4;
  121;
                                       Length 15016;
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US-09-350-756-9
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US-09-350-756-9
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                                                                                                             US-08-955-138-2/c
                                                                                                                                RESULT 13
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LENGTH: 1327
TYPE: DNA
ORGANISM: Clostridium botulinum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/09350756 Patent No. 6495143
                                                      GENERAL INFORMATION:
                                                                      Sequence 2, Application US/08955138A Patent No. 5977435
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TITLE OF INVENTION: Botulinum Neurotoxin Vaccine
FILE REFERENCE: 003/124/SAP RIID 98-21
CURRENT APPLICATION NUMBER: US/09/350,756
CURRENT FILLING DATE: 1999-07-09
EARLIER APPLICATION NUMBER: US 60/092,416
EARLIER FILLING DATE: 1998-07-10
NUMBER OF SEQ ID NOS: 11
APPLICANT: Lefebvre, Daniel D.
APPLICANT: Gellatly, Kevin S.
TITLE OF INVENTION: PLANT PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Michael D. Parker APPLICANT: Jonathan F. Smith APPLICANT: Mark T. Dertzbaugh
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Pred. No. 0.79;
0; Mismatches 102;
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Patent No. 6448043
GENERAL INFORMATION:
APPLICANT: Gil H. Choi
TITLE OF INVENTION: E:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
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US-09-071-035-83
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SEQ ID NO 2
LENGTH: 3981
TYPE: DNA
ORGANISM: SOLANUM TUBEROSUM
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Best Local Similarity 50.0%;
Matches 97; Conservative
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CURRENT FILING DATE: 1997-10-21
NUMBER OF SEQ ID NOS: 119
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          SEQUENCE CHARACTERISTICS:
LENGTH: 1579 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Ver
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                              NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: A. Anders Brookes
                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DAT
APPLICATION NUMBER:
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                                                                                                          TELEPHONE: (501)
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                                                                                                                                                                                                                                         FILING DATE:
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o. 6448043
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                   (301)
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                                                                                                                                                                                                                                                                                                                                                                                                         Diskette, 3.50 inch, 1.4Mb
                                                                                                                 309-8512
                                                                                                                                                                                                                                                                       DATA:
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Pred. No. 1.7;
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US-09-071-035-81
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                                                                                                                   Query Match 0.9%; Score 38.6; DB 4; Length 1680; Best Local Similarity 49.3%; Pred. No. 1.1; Matches 101; Conservative 0; Mismatches 104; Indels 0
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Sequence 81, Apr-
No. 6448043
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Best Local Similarity 49.3
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                         TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: A. Anders Brookes
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: P836
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gil H. Choi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MSDO
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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STREET: ya..
CITY: Rockville
CTATE: Maryland
TCA
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APPLICATION NUMBER:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                          LENGTH: 1680 base | TYPE: nucleic acid STRANDEDNESS: doub
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                           TOPOLOGY:
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                                                                                1501 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA 1560
  1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTTGAAGATGATGGG 1620
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                                          GTAGCAAAAGCATTGCCGATGATTTCAGAAGATGGAAAAACCTACACGATTTCTTTGAGA
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                                                                                                                                                                                                                                                                                    1680 base pairs
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpna/US07 PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06 NEW PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US07 NEW PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/US08 NEW PUB.seq:*

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10: /cgn2_6/ptodata/2/pubpna/US09E PUBCOMB.seq:*

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US-10-027-632-204326

US-10-027-632-204326

US-10-316-253-266

US-10-316-253-266

US-10-316-253-268

US-09-880-107-3727

US-10-006-288-405

US-09-981-151A-9

US-10-094-886-125
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223, App
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48, Appl
12867, Appl
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ALIGNMENTS

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Sequence 1810, Application US/09833381

Patent No. US20020132090A1

GENERAL INFORMATION:
APPLICANT: Robison, Keith E.
TITLE OF INVENTION: No. US20020132090A1el Nu
FILE REFERENCE: 5800-119
CURRENT APPLICATION NUMBER: US/09/833;381
CURRENT FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR APPLICATION NUMBER: 09/516,448
PRIOR FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1810
LENGTH: 3033
TYPE: DNA
CRGANISM: Homo sapiens
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Best Local Similarity 98.0%;
Matches 2648; Conservative
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1816 ACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGGATATTATTTAGGCATG
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Pred. No. 0;
0; Mismatches
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376 TCATCABACTCCAAACTTTCTGACTCCTGGCCACCACGCTCCTGGATATGAAGTTGAA 315 1746 TCATCABAGTCCAAACTTTCTGACTCCTGGCCACCACCTCCCTGGATATGAAGTTGCA 1805 3436 GCCTATGCACTGCTCCACACTTCTTACAATTTCAGACTTCTGAGGGAATCCCAATTATG 3495	56 ACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGATCCTTACATAGATATT

361	Qy 301 ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC	Qy 241 GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG	QY 181 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAGAGAG	Oy 121 AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG	Qy 61 GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA	CACCGCTCCTGACCGCCGCCACCTCC	45.9%; Score 1969.4; DB 12; rity 99.9%; Pred. No. 0; nservative 0; Mismatches 1; In	; LENGTH: 2273 ; TYPE: DNA ; ORGANISM: Homo sapiens US-10-108-260A-953	CURRENT FILING DATE: 2002-03-27 NUMBER OF SEQ ID NOS: 5458 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 953	APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: NO. US20040005560Alel full length cDNA FILE REFERENCE: H1-A0106 CURRENT APPLICATION NUMBER: US/10/108.260A	US-10-108-260A-953 ; Sequence 953, Application US/10108260A ; Publication No. US20040005560A1 ; GENERAL INFORMATION:	Db 2706 TGA 2708 RESULT 2	Qy 4285 TGA 4287	Qy 4225 CACTCTTCAGTCATTTTATTTTCTGTTTCAAGCTTCTGTACTTTATGGAACTTTGGCTG		Db 2526 GAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTGTGAC QY 4165 CTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCAT	4105	Qy 4045 GTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCCATAGTGGATTACTAT	Qy 3985 AAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGTGTTAATATTCCTGCT
	TTCTCTAATAGTACC 360	300 UY 365	240 Qy 1	180 Qy 1	Qy	12	Length 2273; Db 108 dels 0; Gaps 0;	Db 102	QV 9	Оу	. Qy	Qy		ATGGAACTTTGGCTG 4284 Db 6	2645 Qy	2585 . Qy 4224 . Db	4164	4104 Db 2525 Qy	4044 Db 2465 Qy
41 TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA 1500 	BI AGTICTICITAGTAGACATACATICAACTAAAAACAGAGATGAAAATATAAAGTIGGGA 1440 	CTACAGITGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTCATAGICTGTTT	ACTGICCCCAAAGTGAACTTTTAAGATTGAATTCCCAATCCTGAGGATTCCAGTGAG	1 TACTGGAGCGGATCTAACAGTGGAAATCAGAAATGGAAGCTGTTCAGAAAATAAAT	.41 ACTCTTGAAGAAAGAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 1200 	081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC	021 AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTGATTATACTACTGTCTTG 1080 	961 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020 	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	841 ACAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 900 	781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAGAAAATATT 840	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780		66	CTTGGTGACTGATTCAAGTTCAAGTGAATGACCAGACATATTATCAATCA	541 TCACAACAAAGTGAICTIGGAGTCAITTCCAAAACTTTTCAGCTAICTTCCCCATCCAATA 600 606 TCACAACAAAGTGAICTTTGGAGTCAITTCCAAAACTTTTTCAGCTAICTATCTTTCCATCCAATA 666	46 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG	486 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAAGCCTTAC 545 481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540	426 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA

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APPLICANT: ASTROMOFF, Anna
APPLICANT: BARDAMAN, Olga
APPLICANT: BARDAMAN, Olga
APPLICANT: Cocks, Benjamin G.
TITLE OF INVENTION: GENES ASSOCIATED WITH VASCULAR DISEASE
FILE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133,013
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PERL Program
SEQ ID NO 223
LENGTH: 1300
TYPE: DNA
RORANISM: Homo sapiens
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; OTHER INFORMATION: Incyte ID No.
US-10-133-013-223
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US-10-133-013-223
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Best Local Similarity
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Publication No. US20030166903A1
                                                                                                                                                                                                                            Matches 805;
                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                       CTACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATA 3598
CAGAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCT------
                                                                                                                                                                      AGGGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTTGCAT 3538
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                                                                CTACTCAGGATACCACTGTGGCTTTAAAGG---CTGTCTGAATTTGCAGCCCTAATGAATA
                                                                                                                                             AGGGAATCCCAATTATGAGGCGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCAT
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                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                           17.0%;
93.6%;
                                                                                                                                                                                                                        Score 730.8; DB 13;
Pred. No. 4.8e-179;
0; Mismatches 2;
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US-10-160-162-48
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CURRENT APPLICATION NUMBER: US/10/160,162
CURRENT FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/295,558
PRIOR FILING DATE: 2001-06-05
PRIOR PRILING DATE: 1999-01-26
PRIOR PPLICATION NUMBER: CCT/US98/15949
PRIOR PPLICATION NUMBER: CCT/US98/15949
PRIOR PILING DATE: 1998-07-29
PRIOR PILING DATE: 1998-07-29
PRIOR PILING DATE: 1997-07-30
PRIOR PPLICATION NUMBER: 60/054,209
PRIOR APPLICATION NUMBER: 60/054,209
PRIOR APPLICATION NUMBER: 60/054,209
PRIOR PILING DATE: 1997-07-30
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                                                                                                                                                                                                                                                                                                                                                 Sequence 48, Application US/10160162 Publication No. US20030166541A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       FILE REFERENCE: PZ012P2
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: 83 Human Secreted Proteins
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LENGTH: 875
TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 541; Conserv
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FILING DATE: 1997-08-19
APPLICATION NUMBER: 60/056,729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1997-08-18
APPLICATION NUMBER: 60/056,561
FILING DATE: 1997-08-19
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APPLICATION NUMBER: 60/054,213
APPLICATION NUMBER: 60/055,968
APPLICATION NUMBER: 60/055,968
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APPLICATION NUMBER: 60/055,972
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APPLICATION NUMBER: 60/055,969
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                                                                                          TGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCCATAGTGGAGTTACTATG 4105
                                                                                                                                      AACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGTGTTAATATTCCTGCTG
                                                                                                                                                                                                                                             TGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAGTGGAATATGATCATGGAA 3985
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AGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGACC
                      AGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGACC 4165
                                                                                                                                                                         AACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGTGTTAATATTCCTGCTG 4045
                                                                                                                                                                                                              TGCCTTCAGAAGCAATTTCT
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                                                                                                                                                                                                                                                                                                                                                    CTGTAAAAGAAAATAAAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTT
                                                                  TGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATG
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Pred. No. 6.4e-130;
1; Mismatches 0;
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APPLICANT: RUDen et al.
APPLICANT: RUDen et al.
TITLE OR INVENTION: 83 Human Secreted Proteins
FILE REFERENCE: PZ012P1
CURRENT APPLICATION NUMBER: US/09/820,649
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: US/09/236,557
PRIOR FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: PCT/US98/15949
PRIOR FILING DATE: 1999-07-30
PRIOR FILING DATE: 1997-07-30
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,234
PRIOR FILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,218
PRIOR PILING DATE: 1997-07-30
PRIOR APPLICATION NUMBER: 60/054,214
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US-09-820-649-48
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US-09-820-649-48
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SEQ ID NO 48
LENGTH: 875
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Best Local Similarity
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Publication No. US20030199683A1
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Matches 541;
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                         TGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTGGAATATGATCATGGAA 3985
                                                                                                               CGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGCTTTTATGG
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99.8%;
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Pred. No. 6.4e-130;
1; Mismatches 0;
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; FEATURE:
; NAME/KEY: unsure
; LOCATION: (285)
; OTHER INFORMATION: u
; OTHER INFORMATION: C
US-09-960-352-12867
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US-09-960-352-12867
US-09-960-352-12867, Application
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LENGTH: 354
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Best Local Similarity
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 354
TYPE: DNA
ORGANISM: Bos taurus
                    2324
                                                                                     2264
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                                                                                                                                       2204 TAACAACTACTCCAGTGGAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTGAATCTTC
                                                                                                                                                                                                           2144 ATTCTATCACTTCTTGGGTGGCTACTGGTTTTTGTGATCTCTGAGGACCTGGGTCTTGGAC
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                                                                                                                                                                                                                                                                             2084 TTTGGCTAGACACCAACATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTG
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                                                                     CCTACTCTGTTATCAGAGGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTGA
 AAGATGCCACTGAGGTTAAGGTAATCATTGAGAAAAGTGACAAATTTGATAATTCTAATGA 2383
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                                                    CATACTCTGTCATCAGAGGTGAAGAATTTGCTTTGGAAGTAACCATATTCAATTATTTGA
                                                                                                                      GA 4287
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Pred. No. 5.1e-60;
0; Mismatches 36
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US-10-027-632-204326/c
US-10-027-632-204326/c
; Sequence 204326, Application US/10027632
; GENERAL INFORMATION:
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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FILE REPERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

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US-10-7632-204326/c
US-10-7632-204326/c
Sequence 204326, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 204326
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Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                    TTTGCATCTACTCAGG
                                                                                                                                                                       ACTTCTGAGGGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGT
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TTTGCATCTACTCAGG
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Pred. No. 1.3e-39;
0; Mismatches 1;
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Nucleotide

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; SEQ ID NO 204326
; LENCTH: 689
; TYPE: DNA
; ORGANISM: Human
; ORGANISM: Human
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US-10-316-253-266
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         Query Match
Best Local Similarity
Matches 575; Conserv
                                                                              NAME/KEY: CDS
LOCATION: (52)...(45
OTHER INFORMATION:
S-10-316-253-266
                                                                                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 266
LENGTH: 4677
TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 266, Application US/10316253 Publication No. US20030162706A1 GENERAL INFORMATION:
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APPLICANT: Greis, Kenneth
TITLE OF INVENTION: Angiogenesis Modulating
FILE REFERENCE: 8065M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FRACESEQ for Windows Version
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
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                                                                                                                                            FEATURE:
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APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
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                3.0%;
ilarity 47.3%;
Conservative
                                                                                                             (4554)
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             Score 130; Db 13,
Pred. No. 3e-22;
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Pred. No. 1.3e-39;
0; Mismatches 1
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GTGATTCATAGTGAGCTTCAAGGTGGCAATAAAAGTCCAGTAACACTTACAGCCTATATT 3156
                                                                                                                                                         ACATTCGGGGACCGCGGTATGAGGCACAGTCAGGGAAACACTTGGCTCACTGCATTTGTG
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                               GCTTTCAATTGGCTCTCGATGAAACAAAGGGAGAACGGTTGTTTCCAACAGTCTGGATCC
                                                          ACATACACTTGGCTTAAAGGACATCAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGA 3096
                                                                                             CTCAAGGCCTTCGCTCAAGCTCAGTCATACATCTATATAGAAAAGACACACATCACAAAT
                                                                                                                       TTAAGATGTTTCCTTGAAGCCGATCCTTACATAGATATTGATCAGAATGTGTTACACAGA
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; FEATURE:
; NAME/KEY: CDS
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; OTHER INFORMATION:
US-10-316-253-268
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Best Local Similarity 47.3%;
Matches 575; Conservative
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Angiogenesis Modulating
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TYPE: DNA
ORGANISM: Rattus norvegicus
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    GCAACTGTTCTTTTCCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACA 2505
                                                                                                 TCAAGTGAAATAAATGCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGG
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Greis, Kenneth
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b. US20030162706A1
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APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR PILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-06-16
PRIOR FILING DATE: 2000-07-10-02
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APPLICANT: Vockley
APPLICANT: Scherf,
APPLICANT: Gene Lo
                                                                                                                                                                                                                                                                                Sequence 3727, Application Patent No. US20020142981A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 3727
LENGTH: 4615
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                   Sequence 405, Application US/10006285 Publication No. US20030165854A1 GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 405
           APPLICANT: Mary Jane Cunningham
APPLICANT: Matthew R. Kaser
TITLE OF INVENTION: MARKER GENES RESPONDING
FILE REFERENCE: PA-0039 US
CURRENT APPLICATION NUMBER: US/10/006,285
CURRENT FILING DATE: 2001-12-05
NUMBER OF SEQ ID NOS: 514
SOFTWARE: PERL Program
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ilarity 51.6%;
Conservative
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                                                                                                               TREATMENT WITH TOXINS
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Sequence 9, Application US/09981151A
Publication No. US20030212256A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R
APPLICANT: Gerlach, Valerie
APPLICANT: MacDougall, John R
APPLICANT: Malyankar, Muriel M
APPLICANT: Malyankar, Muriel M
APPLICANT: Miltheon, Glennda
APPLICANT: Millet, Isabelle
APPLICANT: Millet, Isabelle
APPLICANT: Peyman, John A

APPLICANT APPLICANT

Shimkets, Richard

APPLICANT:

Malyankar, Muriel N Smithson, Glennda Millet, Isabelle Peyman, John A Stone, David J Gunther, Erik Ellerman, Karen

RESULT 13 US-09-981-151A-9

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Best Local Similarity
Matches 318; Conserv
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TYPE: DNA
ORGANISM: Homo:
FEATURE:
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OTHER INFORMATION:
3438
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                              GAATTCAGTAGAGGAA
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                                                                                         GGATATAGAAAGTATCAGCCTAACATTGATGTGCAAGAGTCTATCCATTTTTTGGAGTCT
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CURRENT APPLICATION NUMBER: US/09/981,151A
CURRENT FILING DATE: 2001-10-16
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TITLE OF INVENTION: Proteins and Nucleic Acids
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APPLICATION NUMBER: 60/242,881
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 TTCAAGTGAAATAAATGCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGG 2444
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                              CCTGGCTAAATCGCATGAGTACCAGCTAGAATCATGGGCAGATTCTCAGACCTCCAGTTG
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Gangolli, Esha A
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Taupier Jr, Raymond
Burgess, Catherine F
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Guo, Xiaojia
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RESULT 14
US-10-094-886-125
; Sequence 125, Application US/10094886
; Publication No. US20040002120A1
; GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh
APPLICANT: Tchernev, Velizar T.
APPLICANT: Liu, Xiaohong
; APPLICANT: Butturajan, Meera
APPLICANT: Butturajan, Meera
APPLICANT: Burgess, Catherine
APPLICANT: Burgess, Catherine
APPLICANT: Li, Li
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LOCATION: (1)..(4309)
-10-094-886-125
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING
FILE REFERENCE: 21402-290 B
CURRENT APPLICATION NUMBER: US/10/094,886
CURRENT FILING DATE: 2002-03-07
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TYPE: DNA
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APPLICATION NUMBER: 60/274,281
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APPLICATION NUMBER: 60/288,052
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APPLICATION NUMBER: 60/274,194
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Pochart, Pascal
Fernandes, Elma
Shimkets, Richard
Rastelli, Luca
Spaderna, Steven
LaRochelle, William
Zhong, Mei, William
                         GGTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACAACTACTCCAGT
                                                                                     CATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATCCTATCACCTTCTTG
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             TTGCCTTGAAGCGGCATTGGACAGTGGTGTCACTAATGGCTATAATCATGCAATTCTAGC
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; LOCATION: (1119)
; OTHER INFORMATION: n equals a,t,9, or
US-09-764-853-362
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US-09-764-853-362
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Best Local Similarity
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: DJZ06
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
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LOCATION: (1018)
OTHER INFORMATION: n equals a,t,g,
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TYPE: DNA
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Search completed: January 17, 2004, 00:35:05 Job time: 1346 secs

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37 K-E	CB158287	14	432	7.4	318.4	43
5936 DKFZp686	59	13	651	7.5	N	42
8463 wq06b02.	84	9	652	7.8	u	41
49 zc36a07	W46849	14	458		33.	40
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3496	CA893496	14	511		38.	38
0 60282	72	12	806	8.1	345.2	37
523 AV245	u	9	684	٠	50.	36
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X472602 DI	X47260	ű	515	۲	496	14
58337 K	B 15	14	613	ŗ	498	13
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ALIGNMENTS

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TITLE JOURNAL MEDLINE	REFERENCE AUTHORS	TITLE JOURNAL MEDLINE	KEYWORDS SOURCE ORGANISM	ACCESSION VERSION	RESULT 1 AK029247 LOCUS DEFINITION
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374	10349636 2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 99279253	HTC; CAP trapper. Mus musculus (house mouse) Mus musculus Mus musculus Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	library, clone:4831440K17 product.weakly similar to alpha-2-macroglobulin (fragments) [Limulus polyphemus], full insert sequence. AK029247. AK029247.1 GI:26081244	AKO29247 4485 bp mRNA linear HTC 05-DEC-2002 Mus musculus 0 day neonate head cDNA. RIKEN full-length enriched

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                                                                                                                                                                                                                                  Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
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Analysis of the mouse transcriptome of 60,770 full-length cDNAs
prepare mouse tissues.
Please visit our web site for further URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
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CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group
Genomic Sciences Center and Genome Science Laboratory in R
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Query Match
Best Local Similarity
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ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG
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                                                                                                     GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT
                                                                                                                                                                                 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAAACTTTTCAGCTATCTTCCCATCCAATA
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                                                                    GTCCTAGAATATGTGTTACCAAAGTTCGAAGTCACCGTGCAGACCCCGCTGTATTGTTCC
                                                                                                                                                          TTTGGTGACTGGTCCATTCAGGTTCAAGTGAATGATCAGCAATATTACCAGTCATTTCAG
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weakly similar to alpha-2-macroglobulin (fragments)
[Limulus polyphemus] (PIR|A36260, evidence: FASTY,
51.8%ID, 76.7%length, match=168)"
a 970 c 1010 g 1228 t
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/clone_Tib="RIKEN full-length
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/db_xref="taxon:10000"
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1783 AGTGTGAATCGATGAATGACCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTG 1842 	1723 TCTCTTAGGATCTCTGTGACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAA 1782 	1663 TTTAAAAATAAGATAAAGCTATATTGGAGTAAAGTGAAAGCTGAAACCATCTGAGAAAGTC 1722 	1603 TATATTGAAGATGATGGGGAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTT 1662 	1543 ACAATGTTCTCTTTAACACCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTAT 1602 	1483 GAGTTAAGCTATATGGTAGTATCCAGGGGACAGTTGGTGGCTGTAGGAAAAACAAAATTCA 1542 	1423 GAAAATATAAAGGTGGGATCGCCTTTTGAGTTGGTGGTTAGTGGCAACGAATCGAAG 1482 	1363 GCAGTTCATAGTCTGTTTAAGTCTCCTAGTAAGACATACAT	1303 CTGGAGGATTCCAGTGAAGCTACAGTTGAAGGCCTATTTCCTTGGTAAAAAGTAGCATG 1362	1243 GTTCAGAAAATAAATTATACTGTCCCCCAAAGTGGAACTTTTTAAGATTGAATTCCCAATC 1302 	1183 CAGAGAAACTATACTGAGTACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCT 1242 	1123 GCTGATGGCAACCAACTGACTCTTGAAGAAAGAAGAATAATGTAGTCATAACAGTGACA 1182 	1063 GATTATACTACTGTCTTGAAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGT 1122	1003 TCAAGAAATGTAAGCACTAATGTGTTTCTTCAAGCAACATGATTACATCATTGAGTTTTTT 1062	943 CTATCTTCCCCTGGACCAGTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATT 1002	901 AATGTAAT	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 900 	829 TTGAAGTCTAAACAGTTAAATGGCTCCGTCATAGCAAAGTATACATAC
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                                       CTTATGGAAGTGAACCTTCTCAGTGGCTTTAGTGCATCTTCAGATTCAATTCCTCTGAGT
                                                                                                                                          AGTCACCTGAATCTGAATGTGTGCACAAGTCACTTGGGTTCAGAGAGGACAGGCATGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Please visit our web site for further details.
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ATTACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGATG
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                                          GATCTATCTTCCCCTGGACCAGTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGT
                                                                                             AAAAAGGTAATGAATTTGAAACCGCTAACGGATGTCTCGGAAGGGAGTTATGAGAATGTG
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2125 TGATTTTGAAGATGCTTCTTCAGTTAACAATGTACATGTCAGGAAGAATTTTCCAGAAAC 2184	AGATATTCATGACTTTTCTTTGGGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGAC	1959 TGTTTATGACAATGCAGAATATGCTGAGAGGGTTTATGGAGGAAAATGAAGGACATATTGT 2018	1899 TCAGGAATGTGGACTCTGGGTATTGACAGATGCAAACCTCACGAAGGATTATATTGATGG 1958	1839 GTTGGAACTTTATAACACAGGATATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTT 1898	1779 CAAAAGTGTGAATCTGATGAATGCCTCTAATGATATTACAATGGAAAATGTGGTCCATGA 1838	1719 AGTCTCTTTAGGATCTCTGTGACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGA 1778	1659 TGTTTTTAAAAATAAGATAAAGCTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAA 1718	GTATTATATGAAGATGATGGGGAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCT	TTCAACAATGTTCTCTTTAACACCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGT	GAAGGAGTTAAGCTATATGGTAGTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAA	1419 AGATGAAAATATAAAGGTGGGATCGCCTTTTGAGTTGGTGGGTAGTGGCAACAAACGATT 1478	CATGGCAGTTCATAGTCTGTTTAAGTCTCCTAGTAAGACATACAT	AATCCTGGAGGATTCCAGTGAGCTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAG	AGCTGTTCAGAAAATAAATTATACTGTCCCCCAAAGTG	GACACAGAAAACTATACTGAGTACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGA	CGTGCTGATGGCAACCAACTGACTCTTGAAGAAAGAAAAAAAA	TTTGATTATACTACTGTCTTGAAGCCATCTCTAACTTCACAGCCACTGTGAAGGTAACT	1000 ATTTCAAGAAATGTAAGCACTAATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTT 1059
QY 3159 AACTTCTCCTCCTGGGATATAGAAAGTATCAGCCTAACATTGATGTGCAAGAGTCTATCCA 3218	Qy 3099 GATTCATAGTGAGCTTCAAGGTGGCAATAAAAGTCCAGTAACACCTTACAGCCTATATTGT 3158	ATATACTTGGCTTAATGCACATAAGAAATTCAATGGTGAATTTTGGGAGCCAGGAAGAGT	3030 ATBCHTCTTTGGAAGCTGATTACAAAATTGATGATGATTTTTGGGATGTTACACAAGAGGT	3025	2859 TCTTTCATTTATGAGCCAAGGTTACCAGAGGAACTTCTCTATCAGAGGGAAGATGCCTC	2799 TIACATTTTGGATTATCTGACTAAAAAGAAACTGACAGATTAATTTGAAAGAAA	2739 ATTGATTCGATGCCTTATGGCTGGAGAGAACATGATAAATTTTGCTCCAAATAT	AGAGTTCAGATCACTGCAATTGGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTC	ACAGAGTACCCTGAAAACTTTGAGTTTCTCATTTCCTCCTATACAGTGACTGGCAGTGA				Qy 2379 AATGACTTCAAGTGAAATAAATGCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGA 2438		Qy 2259 TCTTCCCTACTCTGTTATCAGAGGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTA 2318	Qy 2199 TGGACTAACAACTACTCCAGTGGAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTGAA 2258	Qy 2139 ACCTGATTCTATCACTTCTTGGGTGGCTACTGGTTTTGTGATCTCTTGAGGACCTGGGTCT 2198	Qy 2079 TTGGATTTGGCTAGACACCAACATTGGGTTACCAGGATTTACCAAGAATTTGAAGTAACTGT 2138

 92	4188 CCGTCCTTGTGAGGATCGAGCTTCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTT 4247
מם	4279 AAGCTACAACACCCAGGTGAAGCTGTCCTCGTGTTACCTCAGTCCAGACACCAACTG 4335
γ	4128 AAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGAACCTTTGCAGTGATGTCCAAGGGCTG 4187
рь	4068 TACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAG 4127
ф	159
Qy	4008 TGTAAATGAAACCCAGTTTTGTGTTAATATTTCCTGCTGTGAGAAACTTTTAAAGTTTCAAA 4067
מם	4099 GAGTGAGACCCTGAAGAAAGTGGAATATGATAACGGGAAACTCAACCTTTATTTA
ν2	ATT
Ма В 6	3888 GGCTCTTATGGAAGITAACCTATTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCT 3947
BASI ORIO	3828 TCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGTGGCAT 3887
	3768 ATCTATCCAAAATCAAGAAGCCTTTGATTTAGATGTTGCTGTAAAAGAAAAAATAAAGATGA 3827
	3708 TATTIGICAGCICAAIGIIGIATAIAAIGIGAAGGCIICIGGGICIICIAGAAGACGAAG 3767
FBAC	3652CTTGCTGTGGTACAGCCAATGGCAGTTAATATTTTCCGCAAATGGTTTTGGATTTGC 3707
	3639 CTCACCAAGTCCT 3651
	3579 ATTTGCAGCCCTAATGAATACAGAAAGGACAAATATCCAAGTGACCGTGACCGTGCCCTAG 3638
COM	3519 TAGCTTGGGTGGTTTTGCATCTACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTG
REFI AI	3459 CTTACAATTTCAGACTTCTGAGGGAATCCCAATTATGAGGTGGCTAAGCAGCAAGAAGAA 3518
SOUI	3399 CTCCTGGCAGCCACGCTCCCTGGATATTGAAGTTGCAGCCTATGCACTGCTCTCACACTT 3458
ACCI VBRS	3339 GAGAGCAGAACAAGAAGGTGGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGA 3398
AL59 LOCU	3279 TTATGCATTGTCATCAGTGGGAGTCCTAAAGCGAAGGAAG
Db	325 GTTTTGGAATTTGAATTCAGCAGAGGAATTTCGGACAATTATACCTTAGCAATTATATC
δ	TTTTTTGGAGTCTGAATTCAGTAGAGGAATTTCAGACAATTATACTCTAGCCCCTTATAAC
рь	3265 GACTTCTGTCCTGGGATACAAAAAGTATCAGCCTAATATCGATGTACAAGACTCAATCAA

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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seg=CSODIO81DA09QP1&cluster=1578.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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Contact: Genoscope
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Location/Qualifiers
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GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG
                                                                                              GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGGTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGTTTCAAGCTTCTGTACTTTATGGAACTTTTGGCTGTGA 4287
                                                                  GAGCTGCTCAAGACAGCATCAAAMMTCACTGTCTCTGTMCTGGAAGCAGAAGGAGTCTTT
                                                                                                                                                       AATGTGACTATTGGGGTGGAGCTTCTGGAAMACTGCCCTTMAMAGGTGACTGTGAAGGCG
                                                                                                                                                                                              AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG
                                                                                                                                                                                                                                               GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGAMAGCMCCAGGGATMATCAGGCCCGGAGGA
                                                                                                                                                                                                                                                                                      GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was grimed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCNVSPORT 6 vector. Library was normalized."
a 238 c 236 g 293 t 75 others
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DI081YB18"
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9; Mismatches 14;
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f
                                                                                  Mammalia, Eutheria, Primate
1 (bases 1 to 941)
Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
                                                         Contact: Genoscope
                                                                       Unpublished
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Mammalia; Eutheria; Primates;
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http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAI029ZD07_CS02740_1&cluster=3578.f.
Contact : Feng Liang Email : fliang@llfetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAI029ZD07_CS02740_1.
Location/Qualifiers
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/clone_Tibs strand cDNA was primed with a NotI-oligo(dT)
/note="Tist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the POWSPORT 6 vector. Library was normalized.
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Qy 3387 Db 181 Qy 3447 Qy 3507 Db 301 Qy 3567 Db 361 Qy 3627 Db 421 Qy 3652 Db 481 Qy 3696 Db 481 Qy 3756 Db 601 Qy 3756 Db 601 Qy 3876 Db 721 Qy 3936 Db 721 Qy 3936	Query Match Best Local Similarity 91.8%; Pred. No. 3e-147; Matches 807; Conservative 0; Mismatches 17; Indels 55; Gaps 3; Qy 3207 AGAGTCTATCCATTTTTTGGAGTCTGAATTCAGTAGAGGAATTATACTCT 3266 [http://image.llni.gov http://image.llni.gov plate: LLAM14090 row: p column: 10 High quality sequence stop: 663. location/Qualifiers location/Qualifiers 1879 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="htaxon:9606" /clone="IMAGE:6514905" /tissue_type="leiomyosarcoma" /tissue_type="leiomyosarcoma" /clone_lib="NHH MGC 71" /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. BASE COUNT 248 a 171 c 206 g 253 t 1 others		BU5 N AGE BU5 BU5 BU5 BU5 BU5 MHOM HOM MHOM MAM	Qy 3600 AGAAAGGACAAATATCCAAGTGACCGTGACCGGGCCTAGCTCACCAAGTCCCTCTTGCTGT 3659
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CACACTTCTTACAATTTCAGACTTCTGAGGGAATCCCAATTATGAGGTGGCTAAG 350
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                                                                                                                                                                                GTGGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGGCTTATGGTGCCTTCAGA 780
                                                                                                                                                                                                               GTGGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGCTTTATGGTGCCTTCAGA 3935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTTGCTATTTGTCAGCTCAATGTTGTATATAATGTGAAGGCTTCTGGGTCTTC
ATTINAGATICIGIAAATGAAACCCCAGTITTIG 879
                          -ATTTAGATTCTGTAAATGAAACCCAGTTTTGTG
                                                                                         TTTCTCCTGAGCGAGACAGTGAGGAAAGTGGGATATGATCATGGGAAAACTCAAC
                                                                                                                   TTTCT-CTGAGCGAGACAGTGAAGAAAGTGGAATATGATCATGGAAAACTCAACC 3994
                                                                                                                                                                                                                                                                              AAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTTCGGGCCCGGG
                                                                                                                                                                                                                                                                                                           AAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTTCGGGCCCGGG 3875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GATTTGCTATTTGTCAGCTCAATGTTGTATATAATGTGAAGGCTTCTGGGTCTTC
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978 bp mRNA linear EST 08-MAY-2003 57 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA CSODIO81YB18 5-PRIME, mRNA sequence. piens (human) GI:30457430

:: Genoscope

pe - Centre National de Sequencage

91006 EVRY cedex - France

seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was constructed by Life Technologies, a division of

gen. This sequence belongs to sequence cluster 3578.f piens

ta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

la; Butheria; Primates; Catarrhini; Hominidae; Homo.

ses 1 to 978)

, Gruber,C., Jessee,J. and Polayes,D.

pith cDNA libraries and normalization

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AARCWAAGTGTAAAAGGAAGTACCCAGGATGARAWTWTAATCTCTAAWAGAACAMGCWTA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACCCGCTTA 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAAGACAGCATAAAAAMTWAAAGTATCAGTAATGGAAGAAGAAGAGTMTTTGAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCCMGGGCMTCGGTTTMTGGTGAMAGCMCCAGGGATAATMAGGCACGGAGGAAATGTG
     GAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCTATGAAT 726
                                                                                                                                                                                                                         TCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTGTTCACAA 546
                                                                                                                                                                                                                                                                                                 AAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTACAAAACC 486
                                                                                                                                                                                                                                                                                                                                                       TCATTTGAGACCAAGAGAATATCTGTCTTCATTCAAACAGACAAGGCCTTATACAAGCCA 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGATCTWTTAARAAAAWAAAWAATCAAAAAAAAAWAWAAACAGTGCAGATGARAWTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAGATTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGAAATGTG
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                                                                                 CAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATACTTGGT
                                                                                                                                                             CAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCCATCCAATACTTGGT
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/mol type="mrNA"
/mol type="mrNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="CSODI081YB18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/note="lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="lib" strand cDNA was primed with a NotI-oligo(dT)
/note="lst strand cDNA was primed double-strand cDNA was
/primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
74 a 151 c 179 g 220 t 54 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ028040
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UI-H-CO0-arh-c-08-0-UI.s1 NCI_C
IMAGE:3106526 3', mRNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 667)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                         194
                                                                                                                                       carcinoma, Bladder carcinoma, Brain oligodenroga;
NCI CGAP Sub9 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are CGTC, AACG, GGGCC, GGAAG, TACC, TAACC, ATGC, AGACA, ATCAC. For additional
                                                                                                                                                                                                                                                                                                                                                                                                                               /lab host="DH108 (Life Technologies)"
/clone_lib="NCI_CGAP_Sub9"
/clone="Vector: pT/T3-Pac (Pharmacia) with a modified
/note="Vector: pT/T3-Pac (Pharmacia) with a modified
polylinker; Site_1: EcoR I; Site_2: Not I; tissues:
Cholonic mucosa with Crohns disease, Cholonic mucosa with
ulcerative colitis, Fetal thymus, Cervix, Cervical
adenosquamous carcinoma, Ligament cells, Prostate
                                                                                            TAG_LIB=UI-H-COO
                                                                                                                        information,
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/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:3106526"
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                                                                                                                        bento-soares@uiowa.edu
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     Unpublished
On Feb 16, 2001 this sequence version replaced
Contact: Genoscope
                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
                                                                                                     AL576908 Homo sapiens PLACENTA COT 25-NORWALIZED Homo clone CSODIO81YB18 3-PRIME, mRNA sequence.

AL576908 AL576908 GI:31315187
EST.
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Genoscope - Centre National
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Pred. No. 3.1e-135;
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was Constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO81DA09NP1&cluster=3578.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO81DA09NP1.
Location/Qualifiers
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                                                                                   AACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCCATAGTGGATTACTATGAGCCA
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AGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCATCACTCT
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/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Tst strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR \
sites of the pCMVSPORT 6 vector. Library was normalized.
a 248 c 224 g 321 t 64 others
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/db_xref="taxon:9606"
/clone="CS0DI081YB18"
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Pred. No. 2.9e-133;
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cgi-bin/cluster.cgi?seq=CSIA1021ZB10NP1&cluster=3578.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1A1021ZB10NP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BX386456 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI081YB18 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
Contact: Genoscope
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1 (Dases 1 to 988)
Li,W.B., Gruber;C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                                                                                                                                                                   AGACGAAGATCTATCCAAAATCAAGAAGCCTTTGATTTAGATGTTGCTGTAAAAGAAAAT 3819
                                                                                                                                                                                                                                                              GGATTTGCTATTTGTCAGCTCAATGTTGTATATAATGTGAAGGCTTCTGGGTCTTCTAGA 3759
                                                                                                                                                                                                                                                                                                                                                             TCACCAAGTCCTCTTGCTGTGGTACAGCCAATGGCAGTTAATATTTTCCGCAAATGGTTTT 3699
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AGTGGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGCTTTATGGTGCCTTCAGAAGCA 3939
                                              AAAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAATCTTTTCNNNCCC-GNTANT
                                                                                        AAAGATGATCTCAATCATGTGGATTTGAATGTGTGTACAAGCTTTTCGGGCCCCGGGTAGG 3879
                                                                                                                                           AGACGAAGATCTATCCAAAATCAAGAAGCCTTTGATTTAGATGTTGCTGTAAAAGAAAAT
                                                                                                                                                                                                                                      GGATTTGCTATTTGTCAGCTCAATGTTGTATAATATGTGAAGGCTTSTGGGTCTTCTAGA
                                                                                                                                                                                                                                                                                                                                   TCACCAAGTCCTCTTGCTGGTACAGCCAACGGCAGTTAATATTKCCGCAAATGGTTTT
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/tissue type="PLACENTA COT 25-NORMALIZED"
/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and Ecor V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 133 c 164 g 249 t 58 others
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/mol_type="mRNA"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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12; Mismatches
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UI-H-FG1-bgj-1-22-0-UI.s1 NCI CGAP FG1 Homo
UI-H-FG1-bgj-1-22-0-UI 3', mRNA sequence.
BU624356
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Tissue Procurement: James Martin
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National Cancer Institute, Cancer Genome Anatomy
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1 (bases 1 to 638)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  m Dr. M. Bento Soares, bento-soares@uiowa.edu
primer: M13 FORWARD
                                                                                                                                                                                            /organisms"Homo sapiens"
/mol types"mRNA"
/db xref="taxon:9806"
/clones"UI-H-FGI-bgj-l-22-0-UI"
/tissue_types"Cell lines"
/dev_stages"Adult"
/dev_stages"Adult"
/lab_hosts"BH10B (Life Technologies)"
/clone_libs="NCI_CAAP_FGI"
NCI CGAP_FG1 is a normalized cDNA library obtained them opool of mRNA from 2 cell lines from Enchondroma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated
                                                                                                     /note="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: ECOR I; Site 2: Not I; NCI CGAP FG1 is a normalized cDMA library obtained from a pool of mRNA from 2 cell lines from Enchondroma tissues.
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                                                                                                                 sequence.
AA418644
AA418644.1
EST.
Bukaryota; Metazoa; Chordata; Cro
Mammalia; Butheria; Primates; Cat
1 (bases 1 to 634)
Hillier,L.; Allen,M., Bowles,L.,
                                                                                                                                                                                      AA418644 634 bp mRNA linear zv93f07.rl Soares_NhHMPu_S1 Homo sapiens cDNA clone similar to TR:G534873 G534873 ALPHA-2-MACROGLOBULIN.
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                                                                                Homo sapiens
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TAG_TISSUB-Enchondroma cell line (Mix of EN1 and EN2)
TAG_SED=CGGTCACTC"

TAG_SED=CGGTCACTC"

187 t.
                                                                                                                                     GI:2080463
                                                                                              (human)
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Pred. No. 1.3e~114;
0; Mismatches 1;
                                     Craniata; Vertebrata; Catarrhini; Hominidae;
 Dubuque, T.,
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   Geisel, G.,
                                                          Euteleostomi;
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IMAGE:767365 5'
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Best Local (
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University Scho
4444 Forest Park Parkway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schellenberg, K., Steptoe, M., T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kucaba, T., Lacy, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
GGCTGCCGTCCTTGTGAGGATGGAGCTTCAGGCTCCCATCATCACTCTTCAGTCATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCATGGCTCTTATGGAAGTTAACCTATTAAGTGGCCTTTATGGTGCCTTCAGAAGCAATT
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                                                                                                            GTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGACCTTTGCAGTGATGTCCAG
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                                                                         GTGAGAAGTTACAACTCTGAAGTGAAGCTGTCCTCCTGTGACCTTTGCAGTGATGTCCAG
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="Soares NhHMPu_S1"
/clone lib="Soares NhHMPu_S1"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.B. clones 260232-265223,
340488-345479, and 484488-489479."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:767365"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 525; DB 9; Li
Pred. No. 1.2e-105;
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AUTHORS
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-res@gsc.riken.go.jp,
URL.http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muzamatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagama,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                     Human Genome Sequences. Mamm.
Please visit our web site (ht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000) Konno, H., Fukknishi, Y., Shibata, K., Itoh, M., Carninci, P., Sug
                                                                                                                                                                                                                                                                                                                                                                                           further details.
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/sex="mixed"
/tissue_type="head"
/dev_stage="0 day neonate"
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                                                                                                        /db_xref="taxon:10090"
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Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.

21C Frontier Korean EST Project 2001
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/note="Organ: Liver; Vetcor: pT7T3-Pac; Site_1: EcoRI;
/note="Organ: Liver; Vetcor: pT7T3-Pac; Site_1: EcoRI;
Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="L18POOL1n1-10-H06"
/cell_line="SNU-354+Cho-CK+Choi-CK+HLK-3"
/lab_host="Top10F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
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Pred. No. 1.2e-99;
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RESULT 14
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ORGANISM
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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DKFZp686C02145_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686C02145_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by GBF (National Research Centre for Biotechnology Lt Braunschweig/Germany) within the cDNA sequencing consortium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin-Charlottenburg, GERMAN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sl sequence also available.
This clone (DKFZp686C02145) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14055
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 515)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
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                       AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 180
                                                                                          GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGGATCATCAGGCCCGGAGGA
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                                                                                                                                              ATGCAGGCCCACCGCTGCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG
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                                                                                                                                                                                                                                                                                                                130
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                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                            /clone lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA;
cDNA-collection"
142 c 120 g 123 t
                                                                                                                                                                                                                                                                                                                                                                                      /clone="DKFZp686C02145"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                          11.6%;
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                                                                                                                                                                                                                                       Score 496; DB 13;
Pred. No. 3.3e-99;
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ORGANISM
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BX370169
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                                                                                                 BASE COUNT
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  Query Match 11.5
Best Local Similarity 94.4
Matches 577; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3578.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAGO38ZHO4_CSO3584_l&cluster=3578.f.
Contact: Feng Liang Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSOBAGO38ZHO4_CSO3584_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hoi
1 (bases 1 to 919)
Li,W.B., Gruber; C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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                                                                                                        /Clone="CSODIO81YB18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 213 c 177 g 242 t 2 others
                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                        11.5%;
Score 493.8; DB 13; Length Pred. No. 1.1e-98; O; Mismatches 27; Indels
                                              919;
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	ACTACTGCAGCCGATCTAACAGTCGAAATCAGAAAATGGAAGCTGTTCCAGAAAATAAAT		GAAGCCATCTCTAACTTCACAGCCA-CTGTGAAGGTAACTCGTGCTGATGGCAACCAAC 1138	AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTA-CTGTCTT 1079	GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020	ATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	CAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAAA 901 	AAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAGAAAAATATTA 841 	

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Search completed: January 16, Job time: 7735 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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SUMMARIES

Result No. 000000 a a ი 143.8 143.8 140.8 171.6 167.6 203.8 182 177.4 175 174 232 230 219.6 Score 152.2 151.2 149.8 146.4 143.8 143.8 143.8 .969 Match Query 98.4 74.4 74.3 63.2 63.2 57.1 45.9 3.4 4950 3.4 122013 3.4 164414 3.4 168503 3.4 275699 3.4 337178 3.3 191258 1.8 4678 1.2 251250 1.1 91419 1.1 149597 1300 163577 176144 5603 4620 176144 4579 144589 191258 Length 4560 2629 4715 4578 띪 D83196 AC03727 AL591483 AC034271 AX054954 AX054954 AX118302 GGOVOM AX122084 DME269539 AC1182668 AC1182668 AC1182668 AC1182668 AC012408) RATA113A DME269538) GPIMSPB) RATA113 AC118254 BC036299 BC051037 AB026130 AX534942 AX534944 AC092399 AC092395 AC115484 AE003649 DROSADH08 AY083458 BC052443 HSM805581 AK095888 AC012408 CIN431688 AX083146 AL590428 AX534940 AX537610 ij XELENDO AX537612 AX534936 **4**X534938 AL834478 Homo sapi AK095888 Homo sapi AX083146 Sequence AL590428 Human DNA AC012408 Homo sapi AJ431688 Ciona int D83196 Limulus sp. AC097023 Rattus no AL591480 Human DNA AC034271 Homo sapi AX054953 Sequence AX054953 Sequence AX054954 Sequence AX0123084 Drosophil X78801 G.gallus mR AY122084 Drosophil AJ269539 Drosophil AJ269539 Drosophil AC112668 Mus muscu AC11268 Homo sapi J03552 Rat plasma AJ269538 Drosophil D84339 Cavia porce J03524 Rat alpha-1 L63543 Xenopus lae AC092399 Drosophil AC092395 Drosophil AC115484 Drosophil AC015444 Drosophil AE003649 Drosophil AE003649 Drosophil AE003649 Mus muscu BC036299 Mus muscu BC036299 Mus muscu AX537610 Sequence AX537612 Sequence AX534942 Sequence AX534944 Sequence AY083458 Mus muscu BC052443 Mus muscu Description AB026130 Cyprinus AX534934 Sequence Sequence Sequence

ALIGNMENTS

JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX534934	RESULT 1
Patent: WO 02070696-A 1 12-SEP-2002;	Cd109 nucleic acid molecules polypeptides and methods of use	Schuh, A. and Sutherland, R.D.	1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens (human)		AX534934.1 GI:25261474	AX534934	Sequence 1 from Patent WO02070696.	AX534934 4761 bp DNA linear PAT 22-NOV-2002		

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SRNVSTNVFFKOHDYI I EFFDYTTVLKFSLNFTATVKTRADGROLITLEERRINVVIT
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GVELLEHCPSQVTVKAELLKTASNLTVSVTEAEGYPEKGSFKTLTLPSLPLNSADEIY
ELR-WTGRTQDEILFSNSTRLSFETKRISVFIGTDKALYKPKQEVKFRIVTLFSLPLNSADETY
KTSLNILLKDPKSNLTQOPLSQOSDLGVUSKTFQLSSHPILGDWSIQVQVNDQTYYQS
KTSLNILLKDPKSNLTQOPLSQOSDLGVUSKTFQLSSHPILGDWSIQVTLTFLPLSFWGK
EQVSEYVLPKFEVTLQTPLYCSNNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGK
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VSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHHSSVIFIFCFK
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/mol_type="genomic DNA"
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Homo sapiens CD109 (CD109) mRNA,
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                                                                                              Lin,M., Sutherland,D.R.,
Wu,X.-F. and Schuh,A.C.
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KTQVSEYVLPKFEVTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFMGK
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1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA 1440	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT 1380 	1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1320 	1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	1141 ACTCTTGAAGAAGAAGAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 1200 	1081 AAGCCATCTCTAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC	1021 AATGTGTTCTTCAAGCAACATGATTACATTGAGTTTTTTGATTATACTACTGTCTTG 1080	961 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGATGAAA 900 	781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAGAAGAAATATT 840	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780 	661 GITTCAGAATATGIATTACCAAAATITGAAGTGACTTTGCAGACACCATTATATTGITCT 720	601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAATGACCAGACATATTATCAATCA	541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600	481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540	421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTGAGATTTTTAAGCCTTAC 480	361 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA	
da Ç	g 42	5 B &	S B S	B 8	D 5	Q ₽ Q	ρb	p &	g 40	da Vy	₽ <i>Q</i>	D 49	P &) B &	B &) B &	g 4	§ B
2461 CCCATCAGGCCAACACAT CTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT 2520	#01 GCCALGAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTT	ANGSTANICATIONS MANAMASIGN CAMAITIGATATIC TAMISMIC TO MANGTANATAMAT ANA TAMISMIC TAM	281 GGTGAAGAATTIGCTTIGGAAATAACIATAATTCAATTATTGAAAGATGCCACTGAGGTT 	221 GAGCTCCAAGCCTTCCAACCAFTTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGA 2	161 GIGGETACIGGITITGIGATETETGAGGACCTGGGTCTTGGACTAACAACTACTCCAGIG 2 [101 ATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACTCTATCACTTCTTGG	041 G9TAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAAC 	GCTGAGAGGTTTATGGAGAAAATGAAGGACATATTGTAGATTATCATGACTTTTCTTTG	TIGACAGATGCAAACCTCACGAAGGATTATATTATTGATGGTGTTTATGACAATGCAGAATAT 1	TATTATTTAGGCARGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1	GCTTCTAATGATATTACAATGGAAAATGTGGTCCATGACTTGGAACTTTATAACACAGGA		CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTCTGTG	GAPATIATAAGIJGATGITCTAAAAATTCCTGTTCAGCTTGTTTTTAAAATAAGATAAAGTAAAGATAAAGATAAAGATAAAGATAAAGATAAAAGATAAAGATAAAAGATAAAAGATAAAAGATAAAAATAAGATAAAAGTAAAAATAAGATAAAAGTAAAAAGTAAAAAGTAAAAGTAAAAGTAAAAAA	CAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTAATTGTAGAATGATGATGGC 	GTATICCAGGGACAGTIGGTIGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA 15	TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA 16	AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA

3541 ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA 3600	3481 GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGGATCT 3540	3421 GATATTGAAGTTGCAGCCTATGCACTGCTCTCACACTTCTTACAATTTCAGACTTCTGAG 3480	3361 ATGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGGCAGCCACGCTCCCTG 3420	3301 AGTCCTAAAGCGAAGGAAGCTTTGAATATGCTGACTTGGAGAGCAGAACAAGAAGGTGGC 3360	3241 AGAGGAATTTCAGACAATTATACTCTAGCCCTTATAACTTATGCATTGTCATCAGTGGGG 3300	3181 AAGTATCAGCCTAACATTGATGTGCAAGAGTCTATCCATTTTTTGGAGTCTGAATTCAGT 3240	3121 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCTCTC	3061 CAGAAATCCAACGGTGAATTTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT 3120 	ωμ	2941 GACCCTTCTGGGAGCACTTGGTTGTCAAGCTTTTTTAAGATGTTTCCTTGAAGCCGAT 3000	1 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGGAATTAT 2	AAAAAGAAACAACTGACAGATAATTTGAAAGAAAAAAGTCTTTCATTTATGAGGCAAGGT 2	761 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATCTGACT 2 	13 GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTCGGATGCCTTATGGC 2	641 AGTTTCTCATTCCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT 270 [581 TCACAATCCATCTTATTAGACTTGACTGACAATAGGCTACAGAGTACCCTGAAAACTTTG 2	2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAAGCTGAAGGAATAGAAAAATCATAT 2580
Location/Qualifiers 1. 5895 /organism="Homo sapiens" /mol type="genomic DNA"	AUTITIES Cd109 nucleic acid molecules polypeptides and methods of use JOURNAL Patent: WO 02070696-A 5 12-SEP-2002; Patent: WO 02070696-A 5 12-SEP-2002; Schult: Addrect(A) - Sutherland, Robert D. (CA)	NISM Homo sapiens Sukaryota; Metazoa; Chordata; Cra Eukaryota; Metazoa; Chordata; Cra Mammalia; Butheria; Primates; Cat	ACCESSION AX534938 ACCESSION AX534938 VERSION AX534938.1 GI:25261482 KEYWORDS SOURCE Homo Hapiens (human)	AX534938 5895 bp	Db 4433 ATGGAACTTTGGCTGTGA 4450	4373 TCAGGCTCCCATCATCACTCTTCAGTCATTTTTTTTTCTGTTTCAAGCTTCTGTACTTT	4313 CTGTCCTGTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCTTTTGCAGTGAATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCTTGTTGAGGATGGAGCTTGTGAGGATGGAGCTTGTGAGGATGGAGGTTGTTTTTGAGGATGGAGGTTGTTTTTGAGGATGGAGGTTGTT	4090 ATAGT 4253 ATAGT	4030 GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTCAAATACCCAAGATGCTTCAGTGTCC		TTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTG	QY 3850 GTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA 3909	QY 3790 TTTGATTTAGATGTTGCTGTAAAAGAAAATAAAGATGATCTCAATCATGTGGATTTGAAT 3849	Qy 3730 TATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAATCAAGAAGCC 3789	Oy 3670 AIGGCAGTTAATATTICCGCAAATGGTTTTGGATTTGCTAFTTGTCAGCTCAATGTTGTA 3729	QY 3652	365 377

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AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG
                                                                           AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC
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                                                        AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC
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Query Match Best Local Similarity Matches 4285; Conserv 661 541 481 533 421 473 361 413 301 353 173 113 773 713 601 653 241 293 181 233 121 13 **_** GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT TCACAACAAAGTGATCTTGGAGTCATTTCCCAAAACTTTTCAGCTATCTTCCCCATCCAATA AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGGCCCCGAGGA GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCGCTG GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT CTTGGTGA ANAACCTCTTTAAACATTCTCATTAAGGACCCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG ATGCAGGGCCCACCGCTCAGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG Conservative 98.5%; 0 Score 4222.8; Pred. No. 0; Mismatches B 2 6 Indels Length 4761; 51; Gaps 532 120 832 720 772 660 600 652 540 592 480 420 472 360 412 180 172 60 712 300 352 240 292 232

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AX534940
AX534940.1 GI:25261486
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Homo sapiens
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Mammalia; Eutheria; Primates;
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Andre (CA) ; Sutherland, Robert D. (CA)
Location/Qualifiers
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TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA	ACC 472	413 ATTTA
1381 AAGTCTCCTAGTAAGACATACARCCAACTAAAACAGAGATGAAAATARAAGGTGGGA 1440 	OY	Qy 301 ATTTATGAGCTACGTGTAACCGGACGT
CTACAGITGAAGGCCTATITCCITGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT	CTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 300	Oy 241 GAAAAAGGCTCTTTTAAGACACTTA
1373 ACTGTCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1432	ACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT 240	Qy 181 GAGCTGCTCAAGACAGCATCAAACCTC
1313 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAAATAAAT	GAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 292 Qy	Db 233 AATGTGACTATTGGGGTGG
1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	CIGGAACACIGCCCTTCACAGGTGACTGTGAAGGCG 1	121
1141 ACTCTTGAAGAAGAAGAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 1200	QY	Qy 61 GCCGTGGCTCCCGGGCCTC
	CTCCTCTGCGTGTGCACCGCCGCGCTG 60	Qy 1 ATGCAGGGCCCACCGCTCCTGACCGCCCACCGCTCCTGACCGCCCACACCGCTCCTGACCGCCCCACACCGCTCCTGACCGCCCCACACCGCTCCTGACCGCCCCACACCGCTCCTGACCGCCCACACCGCTCCTGACCGCCCACACACA
1021 ANIGHER LANGUARCA CALIGHTES TACALCALISATIA INCLACTOR THE TOP OF THE TOP	Score 4222.8; DB 6; Length 5895; Pred. No. 0; Db C; Mismatches 2; Indels 51; Gaps 1; Ov	Query Match 98.5%; Best Local Similarity 98.8%; Matches 4285; Conservative
1073 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1132	LLYEMPELML" 1174 C 1241 G 1772 t Db	BASE COUNT 1708 a 1174 C ORIGIN
901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT		YALLSHFLQFQT IQVTVTGPSSES VKASGSSRRRRS LSGFMVPSEALIG

Q	40 40	B 8	Db Qy	₽ <i>Q</i>	₽ &	dg VQ	dg VQ	B &	₽ <i>Q</i>	P Q	Qy db	₽ &	D Q	₽ &	B 8	Qy Db	g dy	σb
3061 CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGGCTTCAAGGT 3120	3001 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3060 	2941 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT 3000 	2881 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGGAATTAT 2940	2821 AAAAAGAAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT 2880 	2761 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATCTGACT 2820 	2701 GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTCGGATGCCTTATGGC 2760 	2641 AGTTTCTCATTTCCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT 2700 	2581 TCACAATCCATCTTATTAGACTTGACTGACAATAGGCTACAGAGTACCCTGAAAACTTTG 2640 	2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT 2580 	2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT 2520	2401 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT 2460	2341 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT	2281 GGTGAAGAATTIGCTTTGGAAATAACTATATTATTATTTGAAAGATGCCACTGAGGTT 2340 	2221 GAGCTCCAAGCCTTCCAACCATTTTTCATTTTTGAATCTTCCCTACTCTGTTATCAGA 2280	2161 GTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACTA		2041 GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAAC 2100	
																		
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4090 ATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAG 4149	GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC	GAAIA GAICA GAAAC ICAAC ICAAIIAA GAIAC GAAIA GAAAC CAGIII IG			953		ATGGCAGTTAATATTTCCGCAAATGFTTTGGATTTGCTATTTGTCAGCTCAATGTTGTA		713		593		473	413	353		233	173 121

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Mammalia; Eutheria;
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KSSMAVHSLFKSSSKTYIQLKTRDENIKYGSPELVVGSKRKLKELSYMVVSRGQLVA
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LALITYALSSYGSPKAKEALNYLTWRAEQEGGWQFWSSESKLSDSWQPRSLDIEVAA
YALLSHFLQFOTSEGIF DIRMYLSRGKRASTQDTTVALKALSEFAALMYTERU
IQVTVTGPSSPSPVKFLIDTHNRLLLQTAELAVVQPMAVNISANGFGFAICQLNVVYN
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LSGFMVPSEA I SLSETVKKVEYDHGKLNLYLDSVNETQFCVN I PAVRNFKVSNTQDAS
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                     AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG
                                                                                                      GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT
                                                                                                                                                                          ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA
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ATGGAACTTTGGCTG 4284
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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GATATTGAAGTTGCAGCCTATGCACTGCTCTCACACTTCTTACAATTTCAGACTTCTGAG 3480	ATGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGGCAGCCACGCTCCCTG 3420	AGTCCTAAAGCGAAGGAAGCTTTGAATATGCTGACTTGGAGAGCAGAACAAGAAGGTGGC 3360	AGAGGAATTTCAGACAATTATACTCTAGCCCTTATAACTTATGCATTGTCATCAGTGGGG 3300	TTCAGT 3	GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCTCCTGGGAȚATAGA 3180 AAGTATCAGCCTAACATTGATGTGCAAGAGTCTATATTGTAACTTTTTTGGAGTCTGAAGTCTGAATTCAGT 3240	GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCCTCCCTGGGATATAGA 3180	CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT 3120	CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3060	CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3060	GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT 3000	, N	TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGGAATTAT 2940	AAAAAGAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT 2880	CAAGGT 2	TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATCTGACT 2820	2	GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTCGGATGCCTTATGGC 2760	AGTITICTATITICS COLLATION OF CONTROL OF CONT	CAATT 270		2 0	CTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT 25	CCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT 25	CCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGGCTCTTTCACCCACT 25	GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTT 2460	GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT 2460
ORGANIS	ACCESSION VERSION KEYWORDS	RESULT I AX53494: LOCUS	Db .	Q B	Q	B 9	DЪ	8 8	ş .Ş	р В	δ	Db !	ο Β	Ş	Db	Q .	유 원	рь	γQ	Дb	γQ	Db	Q	ממ	5 8	; 5
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REFERENCE

Homo sapiens (human) Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1

AX534942 3535 bp Sequence 9 from Patent WO02070696. AX534942 AX534942.1 GI:25261490

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RESULT 8	Db	γ	DЬ	Ş	Db	Ş	Dъ	Ş	Дb	δ	Db	Qy	ДЬ	γQ	Дb	γQ	Db	Q	Db	γQ	Db	Ş	Дb	Ş	дь	Ş	Дb	δ	ф	Ş
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	ATGGAACTTTGGCTG 4335	ATGGAACTTTGGCTG 4284	TCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTCAAGCTTCTGTACTTT 4	TCAGGCTCCCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAGCTTCTGTACTTT 4	CTGTCCTCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT 4	CTGTCCTCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT 4	ATAGTGGATTACTATGAGCCAAGGAGACACGGCGGTGAGAAGTTACAACTCTGAAGTGAAG	ATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAG	()-	GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC 4	GAATATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGT	GAATATGATCATGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTTGT 4	TTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTG 4	TTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTG 3	GIGIGIACAAGCITTTCGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA 3	GTGTGTACAAGCTTTTCGGGCCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA	TTTGATTTAGATGTTGCTGTAAAAGAAAATAAAGATGATCTCAATCATGTGGATTTGAAT	TITGATTTAGATGTTGCTGTAAAAGAAATAAAGATGATCTCAATCATGTGGATTTGAAT 3	TATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAATCAAGAAGCC 3	TATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAAATCAAGAAGCC 3	ATGGCAGTTAATATTTCCGCAAATGGTTTTGGATTTGCTATTTGTCAGCTCAATGTTGTA 3	ATGGCAGTTAATATTTCCGCAAATGGTTTTGGATTTTGCTATTTGTCAGCTCAATGTTGTA 3	CTGATTGACACACACACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGTGGTACAGCCA 3	CTTGCTGTGGTACAGCCA 3	GAAAGGACAAATATCCAAGTGACCGTGACGGGCCCTAGCTCACCAAGTCCTGTAAAGTTT 3	GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCT 3	ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA 3	ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA	GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT 3	GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT 3
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533 AAGCCAAAGCAATCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540		301 ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC 360	241 GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 300	181 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT 240	121 AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 180	61 GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGAGGA 120	1 ATGCAGGGCCACCGCTCCTGACCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG 60	Watch 74.4%; Score 3187.4; DB 6; Length 3535; Local Similarity 100.0%; Pred. No. 0; Local Similarity 100.0%; Pred. No. 0; nes 3188; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	1108 a	ELQAFOPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSNE INATCHQQTLLVPSBDGATVLFFIROTHLGSIF BITVTRALSFTASDAVTQMILVKAEGI EKSYSQSILLDLTUNRLQSTLKTLSFSFPENTVTGSERVQITAIGDVLGPSINGLASL IRMPYGCGBQNMINFAPNIYILDYLTKKKQLTDNLKEKALSFMRQGYQRELLYQREDG	VGKQNSTMESLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVEKNKIKLYWSKV KAEPSEKVSLRISVTQDDSIVGIVAVDKSVYLMANASNDITWENVVHELELVNTGYYLG MFMNSFAVYQECGLWVLTDANITKDYIDGVYDNAEYAERFMEENEGHIVDIHDFSLGS SPHVKHFPETWIKLDTNMGYRIYQEFEVTVPDSITSWYANGFYLEBEDLGLGLTTTPV	KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGI SRAVSTNVFFKOHDYILEFFDYTTVLKPSLNFTATVKVTRADGNOLTLEERRUNVVIT VTQRNYTEYMSGSNGSNQKMEAVQKINYTVPQSGTFKIEFPILEDSSELQLKAYFLGS KSSMAVHSLFKSPSKTYIOLKTRDENIKVGSPFELVVSGRKRIKKELSYMVVSRGOLVA	GVELLEHCPSQVTVKAELLKTASNLTVSVLEAEGVPEKGSFKTLTLPSLPLNSADEIY ELRVTGRTQDEILFSNSTRLSFETKAISVFJQTBKALYKPKQEVKERIVTLPSDFKPY KTSLNILIKDPKSNLIQQMLSQVGJGTGTSKTFQLSSHPILGDMSJQVQVNDQTTYQS FOVSEYVLDKFEVFLOTPLYCSMNSKHLNGTTTAKYTYKGRVTLTFF,PLSFMGK	/codon_start=1 /proteIn_id="CAD57235.1" /broteIn_id="CAD57235.1" /db_xref="GI:25261491" /translation="MGGPPLITAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTI	/mol_type="genomic DNA" /db_xref="taxon:9606" 1133316 /note="unnamed protein product"	Location/Qualifiers 13535 /organism="Homo sapiens"	Schuh, A. and Sutherland, R.D. Cd109 nucleic acid molecules polypeptides and methods of use Patent: WO 02070696-A 9 12-SEP-2002; Schuh. Andre (CA) - Sutherland Bohert D (CA)
QV DB	Db A	S B &) B Q	р р	Qγ	д У	Qγ	dd 49	Db Qy	Qy Db	Qy Db	D Qy	dg VQ	Db Qy	g Qy	Db 43	ָרָ Db
1613 GTATCCAGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTTTAACA 1672 1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGAGGG 1620	1501 GTATCCAGGGGACAGTTGGTGGTGTGGAGAAAACAAACTATCAACAATGTTCTCTTTAACA 1560	AGTCTCCTAGTAAGACATACATCCAACTAAAACAGAGAGAG	321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCAGGCAG	ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG	1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	ACTCTTGAAGAAAGAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG	1081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGGTGATGGCAACCAAC	ARTGIGITCITICAAGCAACAIGATTACATGAGTITTTIGATTATACTACTGTCTTG	GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAGAGATGAAA 900 	781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAGAAGAAAATATT 840 	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780	661 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT 720	601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAATGACCAGACATATTATCAATCA	653 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 712	ADACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAAT

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                     AGTTTCTCATTTCCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGA
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KSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKRLKELSYMVVSRGQLVA
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/codon_start=1
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BASE COUNT ORIGIN Query Match
Best Local Similarity
Matches 3187; Conser 109 653 773 661 541 593 481 533 473 893 781 833 721 713 421 361 413 301 353 241 293 181 233 121 173 113 61 ب ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA AAGCCAAAGCAAGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGAGGA ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCTCTGCGTGTGCACCGCCGCGCTG GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT TCACAACAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCCATCCAATA AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT **AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG** AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG ATGCAGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCCTGCGTGCACCGCCGCGCGCTG AAAGGAGACGTTAACGTTTTTTTACCTTTATCCTTTTTGGGGAAAGAAGAAAATATT 1107 Conservative VGKQNSTMFSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKV
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GRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQVFRI" 74.3%; 99.9%; 0 Score Pred. Mismatches No. 0; В 2 6; Indels Length 0 Gaps 600 840 712 300 120 780 832 772 660 652 540 592 480 532 420 360 412 240 232 172 952 892 720 472 352 292 180 60 0 밁 S 밁 Ś 망 Ś 밁 Ś 밁 Ś 밁 Ś 밁 Ś 밁 8 밁 \$ 밁 S 밁 5 밁 δ 片 Ś 밁 8 문 S 밁 Ş 밁 Ś 밁 S 1973 1913 1861 1801 1853 1741 1793 1681 1733 1621 1673 1561 1613 1501 1553 1441 1493 1381 1433 1321 1373 1261 1313 1201 1253 1141 1193 1081 1133 1021 1073 1013 1921 961 901 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1920 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAAATCTGATGAAT ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT GAAATTATAAGATGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAAATAAGATAAAG GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA AAGTCTCCTAGTAAGACATACATCCAACTAAAAAACAAGAGATGAAAATATAAAGGTGGGA CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG ACTCTTGAAGAAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG ACTCTTGAAGAAGAAGAATAATGTAGTCATAACAGTGACACAGAGAGAAACTATACTGAG AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGATGAAA TTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTATGACAATGCAGAATAT 1980 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAAG CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATTTGAAGATGATGGG GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAAAAAAATTCAACAATGTTCTCTTTAACA TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAGTAGCATGGCAGTTCATAGTCTGTTT ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG **AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG** GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1200 2032 1972 1860 1912 1800 1740 1792 1680 1672 1560 1612 1500 1552 1440 1492 1380 1432 1372 1260 1140 960 1012 1852 1620 1320 1312 1252 1080 1020 1072 1132

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graduate School of Medicine,
Aichi 466-8550, Japan
Location/Qualifiers
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AY083458
AY083458.1 GI:2007
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Hashimoto, M., Ichihara, M. and Takahashi, M
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Mus musculus GPI-anchored alpha-2 macroglobulin-related protein
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                 IGMPMNSFAVFOECGLWALIDATLIRDS IDEVADTEEYSER PAEENEANLVDFEDASS
VNNVHYRKNF PETWIWLDAYMGSKIYEEF EYTVYDST TSWASAF VL SEDLGFCLTTV
PAELQAFQP FFLFLNLEYSVIRGEEFALEVSIVNYLKDTIKVVILIESDSFDILMTS
UDTWGTIYKTVOVPROMOVILVP FIKPTHLGEIP ITVTAASPTASDAVTQTIVVKPE
GIEKSYSKSVLLDLTDSNVESKOQSMRFSFPDTVIGSERVQITAIGDILGSSINGLS
SLIRMFYGCGEOMMIY BAPNIYILDYLTKQKQLTVNLKEKALSYMRQGYQRELLYQRE
DGSFSAFGDIDSSGSTWLSAFVLRCFLEADYYLDIDDQDVLHRTYTMLAHKKFNGEFW
EPGRVIHSELQGGTKSPWTLTPAYIVTSVLGYKKYQPNIDVQDSIKFLEFEFSRGISDN
YTLAIISYALSTVGSPKAEEALNLLMQRSEKEGDTQFWLSSGPALSGSWQPRSVDIEI
AAYALLAHTLHHVSEGIPVMWILIQQBNSLGGFVSTQDTVVALKALSEFSALVHKENT
                                                                                                                                                                                                                                                                                                QVLEYVLPKFEVTVQTËLYCSLKSKQLNGSVJAKYTYGKPVKGSLŠLTELPLSFWKK
KNITKSTEINGFANFSEDNYEMKKVMILKPLTDSLEST
SLTGLSEMASTRIVFFKQDYIIEIFDYTTVLKEDSLSESTATVKYSRSDGNQLTBEETU
DLVTVVTQRKNNHPESQRDQEMDYIQTVNYTIPQNGIIKIEFPVMSISGELQLKAYFL
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VAAGKQSSTTFSLTERASMAPKACIIAYIALBGEIIKDIKIPQULVESKIVELEST
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TSVDIFIKDFKSNVIQQWFSQKGDLGVVSKTFQLSSNFIFGDWSIQVQVNDQQYYQSF
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db_xref="GI:20070080"
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D	04 P P D	Q B Q B :	S & S	ט אס	Q B Q	da Vy	δ δ	D Q	dg VQ	B &	η σ	Db
	2011 TITGAAAATAAGGTAAAGCTGTTTTGGAGTAAACCTACAGTCAAGCCATCTGATAAGGTC 2070 1723 TCTCTTAGGATCTCTGTGACACAGCCTGACTAGTTGGGATTGTAGCTGTTGACAAA 1782	91 AGAACTTTCTCTTTAACACCAGAGGCTTCCTGGGCTCCAAAGGCCTGTATAATCGCATAT 91 AGAACTTTCTCTTTAACACCAGAGGCTTCCTGGGCTCCAAAAATTCCCTGTTCAGCTTGTT 103 TATATTGAAGATGATGGGGAAATTATAAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTT 1	1483 GAGTTAAGCTATATGGTAGTAICCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCA 1542	1711 ACAGTCCACAGTATGTTCACCTCTCCTAGTAAGACGTACATCCAGGCTTAAAACCAGAGAT 1770 1423 GAAAATATAAAGGTGGGATCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAG 1482	1303 CTGAGGATTCCAGTGAGCTACAGTTGAAGCCTATTTCCTTGGTAGTAGAAGTAGCATG 1362	43 GTTCAGAAATTATACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATC	1183 CAGAGAAACTATACTGAGTACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCT 1242	1123 GCTGATGGCAACCGACTGACTCTGAAGAAAGAAGAATAATGTAGTCATAACAGTGACA 1182	1063 GATTATACTACTGTCTTGAAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGT 1122	1003 TCAAGAATGTAAGCACTAATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTT 1062	1300 CCGTCCTTTCCTGGGCCGGCAAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATT 1002	40 AAGGTAATGAATTTGAAACCGCTAACGGATGTCTCGGAAGGGAGTTATGAGAATGTGGAC

3043 ACTIGGCTIAAAGACATCAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATT 3102 	TGTTTCCTTGAAGCCGATCCTTACATAGATATTGATCAGAATGTGTTACACAGAACATAC	AGTGCTTTTGGGAATTATGACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGA 	TCATTTATGAGGCAAGGTTACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTC	ATTTTGGATTATCTGACTAAAAAGAAACAACTGACAGATAATTTGAAAGAAA	ATTCGGATGCCTTATCGCTGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTAC 2 	2683 GTTCAGATCACTGCAATTGGAGATGTTCTTTGGTCCTTCCATCAATGGCTTAGCCTCATTG 2742	2623 AGTACCCTGAAAACTTTGAGTTTCTCATTTCCTCCTAATACAGTGACTGGCAGTGAAAGA 2682	2563 GGAATAGAAAAATCATATTCACAATCCTATATTAGACTTGACTGAC	ACAGCTCTTTCACCCACTGCTTCTGATGCTGCACCCAGATGATTTTAGTAAAGGCTGAA	2443 GGGGCAACTGTTCTTTTTCCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTC 2502	ACTTCAAGTGAAATAAATGCCACAGGGCACCAGCAGGAGCCCTTCTGGTTCCCAGTGAGGAT 2	AAAGATGCCACTGAGGTTAAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATG 2	CCTACTCTGTTATCAGAGGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTG 2	TAACAACTACTCCAGTGGAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTTT	APTICATION	ATTIGGCTAGACACCAACAIGGGTTACAGGATTTACCAAGAATTIGAAGTAACIGTAACCI	2023 ATTCATGACTTTTCTTTGGGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGG 2082
Qy Db	& & &	. Db	9d Qy	B &	Db Qy	B 8	B &	Qy db	Qy dd	D Q	B &	Db Qy	Qy Db	Qу	Qy	D Qy	D Qy
4465 CGAGATGGTTCAGTATCTGTAATGGACTACTATGAACCAAGGACAGGCAGTGCGAAGC 4524 4132 TACAACTCTGAAGGTGAAGCTCCTCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGT 4191	4012 ANTGARACCCAGTTTTGTGTTARTATTCCTGCTGTGAGAACTTTAAAGTTTCAAATAC 4071	GAGACAGTGAAGAAGTIGGAATATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTA	3892 CITATGGAAGTTAACCTATTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGC 3951	3832 AATCATGTGGATTTGAATGTGTGCACAAGCTTTTCGGGCCCGGGTAGGAGTGGCATGGCT 3891	3772 ATCCAAAATCAAGAAGCCTTTGATTTAGATGTTGCTGTAAAAGAAAATAAAGATGATCTC 3831 	3712 TGTCAGCTCAATGTTGTATAATGTGAAGGCTTCTGGGTCTTCTAGAACACGAAGATCT 3771			GCAGCCCTAATGAATACAGAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCA	3523 TTGGGTGGTTTTGCATCTACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTG	TCAGACTTCTGAGGGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGC 		3343 GCAGAACAAGAAGGTGGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCC 3402	3283 GCATTGTCATCAGTGGGGAGTCCTAAAGCGAAGGAAGCTTTGAATATGCTGACTTGGAGA 3342 	3223 TTGGAGTCTGAATTCAGTAGAGGAATTTCAGACAATTATACTCTAGCCCTTATAACTTAT 3282 	3163 TCTCTCCTGGGATATAGAAAGTATCAGCCTAACATTGATGTGCAAGAGTCTATCCATTTT 3222	3103 CATAGTGAGCTTCAAGGTGGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACT 3162

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RESULT 11
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                                                                                                                               Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,J., Bair,J., Crouch,K., Davis,A.,
Fishler,K., Keppel,C., Xucaba,T., Lebeck,M., Melo,A., Schaefer,K.,
Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J.,
Casavant,T., Soares,M.B.
                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
Tissue Proparation: M. Bento Soares, University of Iowa
cDNA Library Preparation: M. B. I. M. A.G. E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (15-MAY-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus
                            Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: Plate: Row: Column: 0.
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Eukaryota; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MGC help desk
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Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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BC052443.1 GI:30851465
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  Plate: Row: Colum
Location/Qualifiers
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Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Best Local S
Matches 3393
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ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC 360
                                                                                                                                                                  CACAGAGGCCATTTCAAGACTCTCGTTCTTCCGGCACTACCTCTGAGCAGTGCAGATAAG
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                                                    ATTTATGAGCTACACATAAACGGACAATCAGAGAATGAGATCGTATTCTCCAACAGGACA
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DIQLTVTGPGI PRS I HFR I DSQNLFLLHQEELHALDP I TVNVSAHGSGFA I CQLNVDY
NVKGSGSSKRRRSTENQEVFDLDV I VNNEDDI SHLNLNVCTSHLGSERTGMVLMEVNL
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DGSFSAFGDIDSSGSTWLSAFVLRCFLEADYYIDIQDVYLHRIYTWLNAHKKFNGEFW
EPGRVIHSELQGGTKSPVTLTAYIVTSVLGYKKYQPNIDVQDSIKFLEFEFSRGISDI
YTLAIISYALSTVGSPKAEEALNLLMQRSEKEGDTQFWLSSGPALSGSWQPRSVDIEI
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SLTGISMASTNVFFKQHDYIIEIFPYTLKESLMFTATFKYSRSDGNQLTPEEIEN
DLYTVTORKNNHPESGDADEMSJCIOTVNTIFQNGIIKIEFPYWSIGGELQLKAYFI
DGTSSVTVHSMFTSPSKTYIQLKTRDEYIKVGSPFDLMVSGNRQFKDLSYMVISKGQL
VAAGKQSKRTPSLTPEASWAPKACIIAYYIAEDGEIIMDILKIPUQLVFENKVKLFWS
KPTVKPSDKVSLRISATQSDSLVGIVADKSVTLMENSKITMETMVHELELYNTEYY
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KNTVKPSDKVSLRISATQSDSLVGIVADKSTVTEYY
LGMFMNSFAVFQECGLWYLTDATLIRDSIDEVLDTEXYSEFFAEENEAHLVDFEDASS
VNNVHRKNEFETFWYMLDAYMGSKIYEEFETVPDESITSWVAGAFVISEDLGGICTTV
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VSVMDYYEPRRQAVRSYNTQVKLSSCYLSPDTNCKSHTDGATDSLRRSSSLLVFCSVL
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NDTNGTIYRKTVQVPRDNGVTLVFPIKPTHLGEIPITVTAASPTASDAVTQTIVVKPE
GIEKSYSKSVLLDLTDSNVESKQQSMRPSFPPDTVIGSERVQITAIGDILGSSINGLS
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HINOGSENEIVFSNRTRLTFESKSISVLIQTDKAFYKEKGEVKFRVLTLCSDLKEYF
TSVDIFIKDDKSNVLQOWFSQKGDLGVVSKTFGLSNRDIFGDWSIQVVOXDQXYVSF
QVLEYVLPKFEVTVQTPLYCSLKSKQLNGSVIAKYTYGKPVKGSLSLTFLPLSFWGKK
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/db_xref="GI:30851466"
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/tissue_type="Brain, enriched mov
/clone_lib="NIH_BMAP_F00"
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/strain="C57BL/6"
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Pred. No. 0;
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2503 ACAGCTCTTTCACCCACTGCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAA 2502	Db Gy	1423 GAAAATATAAAGGTGGGATCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAG 1482
GGGGCAACTGTTCTTTTCCCATCAGGCCAACACATCTGGGAAGAATTCCTATCACAGTC	ДУ	1363 GCAGTTCATAGTCTGTTTAAGTCTCCTAGTAAGACATACAATCCAACTAAAAACAAGAGAT 1422
ACTTCAAGTGAAATAAATGCCACAGGCCACCAGTGAGACACCCTTGTTGGTTCCCAGTGAGGAT 2	B Q	1303 CTGGAGGATTCCAGTGAGCTACAGTTGAAGGCCTATTTCCTTGGTAGAAAAGTAGAAGT 1362
	Qy Ob	GTTCAGAAAATAAATTATACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATC
2263 CCCTACTCTGTTATCAGAGGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTG 2322 	Db Qy	CAGAGAAAATAACTGAGTACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAAGCT
2203 CTAACAACTACTCCAGTGGAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTGAATCTT 2262 	Qy Db	GCTGATGGCAACCAACTGACTCTGAAGAAAAAAAAAATGTAGTCATAACAGTGACA
2143 GATTCTATCACTTCTTGGGTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGA 2202	Ωу	GATTATACTACTGTCTTGAAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGT
2083 ATTTGGCTAGACACCAACATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCT 2142	Qy Db	TCAAGAATGTAAGCACTAATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTT
2023 ATTCATGACTTTTCTTTTGGTAGGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTTG 2082	B &	CTATCTTCCCCTGGACCAGTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATT
1963 TATGACAATGCAGAATATGCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGAT 2022 	B &	901 AATGTAATGATTCTTCAAATGGACTTTCTGAATACCTGGAT 942
1903 GAATGTGGACTCTGGGTATTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTT 1962 	p Q	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 900
GAACTTTATAACACAGGATATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAG 	dg dg	
	B &	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780
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TTTAAAATAKAKTAAAGCTATATATTGAATAAGTGAAAGCTGAAGCCATCTGAGAAAAGTTTTGAAAAATAAGGTCAAGCCATCTGATAAGGTCTTTTGGAGTAAACCTACAGTCAAGCCATCTGATAAGGTC	DB GS	601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAATGACCAGACATATTATCAATCA
TATATTGCAGAGGTGGGAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTT TATATTGCAGAGGATGGGGAAATTATAAATGATATTCTAAAAATCCCCGTTCAGCTTGTT	B &	541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600
ACARTGITCTCTTTAACACCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTAT A) B &	481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540
GROTTANGCTATATIGGTAGTATICANGGGACAGTIGGTGGCTGCAGGCAAACAAAATTCA 1	B 8	421 AAGCCAAAGCAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC 480
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REFERENCE AUTHORS TITLE JOURNAL COMMENT SOURCE ORGANISM

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RESULT 12
HSM805581
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS Homo sapiens mRNA; cDNA AL834478 AL834478.1 GI:21740252 Homo sapiens (human) 2938 bp mRNA linear PRI 12-JUL-2002 DKFZp762L1111 (from clone DKFZp762L1111).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

CE 1 (bases 1 to 2938)

Blum, H., Bauersachs, S., Mewes, H.W., Weil, B. and Wiemann, S. Direct Submission

Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s. Wiemann@dkfz-heidelberg.de; sequenced by LMU (Ludwig Maximilians University, Munich/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZ)76ZL1111) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available

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Matches 2511; Conserv
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ACTGTACCTGATTCTATCACTTCTTGGGTGGCTACTGGTTTTTGTGATCTCTGAGGACCTG 2193
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                                                                            GAGACTTGGATTTGGCTAGACACCAACATGGGTTACAGGATTTACCAAGAATTTGAAGTA
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Location/Qualifiers
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GSTWLSAFVLRCTELADPYIDIDQNVLHRTYTWLKGHGXSNGEFWDPGRVHSELQGG
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SPVKFLLDTHNRLLLQTABLAVVQFTAVNISANGFGFAICQLNVYNVKASGSSRRR
SIQNQBAFDLDVAVKENNDDLNHYDLNVCTSFSGFGRSGNALMSYNLLSGFWVSESRA
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QAVRSYNSEVKLSSCDLCSDVQGCRPCEBGASGSHHHSSVIFIFCFKLLYFMELML"
2843. 2848
//GRNe-STAG21111"
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/hl08; sites NotI + SalI"
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan

(B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Sconomy, Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB, annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K., Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamateu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Isogai, T. and Yamamoto, J.
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Homo sapiens cDNA FLJ38569 fis,
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                                                                                                                                      /translation="MQCPPLLTAAHLLCVCTAALAVAPGPRFLYTAPGIIRPGGNVTI
GVELLEHCPSQVTVKAELKKTASNLTYSVLEAEGVFEKGSFKTITTLPSI;PLNSADEIY
ELRVTGRTQDEILFSNSTRLSFETKRISVFIQTDKALYKSPKQEVKFRIVTLFSDFKPY
KTSLMILKDPKSNLTQOWLSQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQS
FQVSEYVLPKFEVTLQTPLYCSMNSKHLNGTITAKYTYGKPVKGDVTLTFLPLSFWGK
KKNLTKTFKLNGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGFVEILTTVTESVTGI
SRNVSTNVFFKQHDYIIFFDYTTVLKPSLNFTATVKVTRADGNQLTLEERRNNVVIT
VTQRNYTEYNGGSNSGNOKMEAVQKINYTVPQSGTFKLEFPILEDSSELQLKAYFLGS
KSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKRLKELSYMVVSRGQLVA
VGKQNSTMFSLTPENSMTPKACVIVYIEDDGEIISDVLKIPVQLVFKNKIKLYWSKV
VAEPSEKVSLRISVTQPDSIVGIVAVDKSVNLMNASNDITMENVVHELELYNTGYYLG
MFMNSFAVFQBCGLWVLTDANLTKDYIDGVYDNLFGTQEAL"

12 a 431 c 462 g 668 t
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/clone_lib="HCHON2"
/note="cloning vector: pME18SFL3-primary culture,
chondrocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/protein_id="BAC04642.1"
/db_xref="GI:21755237"
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/db_xref="taxon:9606"
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901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	66 ANGCAGGGCCCACCGGCTCCTGGTTTTCGGTGACCGCCCGCGGGGATCATCAGGCCCGGGGGA 125 61 GCCGTGGCTCCCGGGCCTCCGGTTTCTGGTGACCACCCCCAGGGATCATCAGGCCCGAGGGA 126 126 GCCGTGGCTCCCGGGCCTCCGGGTTCTCGGTGACCACCCCCAGGGATCATCAGGCCCGAGGGA 126 127 AATGTGACTATTGGGGTGAAGCTTCTGGTAACACTGCCCTTCACAGGTGACTGAC
RESULT 14 AX083146 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	Qy 112 Qy 12 Qy 12 Qy 13 Qy 13 Qy 13 Qy 13 Qy 14 Qy 14 Qy 15 Db 16 Qy 16 Qy 16 Qy 16 Qy 17
AXO83146 AXO83146 Sequence 49 from Patent WOO110903. AXO83146.1 GI:13185055 Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 Yue,H., Lal,P., Tang,Y.T., Bandman,O., Baughn,M.R., Azimzai,Y., Lu,D.A. and Yang,J. Proteases and protease inhibitors	1141 ACCCTTGANGANAGNANTANTGTAGTCATAACAGTGACCCAGAAGAAACTATACTGAG 1200 1201 TACTGGACGAACTAACAGTGGAAATTAATGTAGCTGTACCAGAGAAACTATACTGAG 1201 1202 ACTGGACGGATCTAACAGTGGAAATTAATGTAGAATTGCAAAGTGGAAGCTGTTCAGAAAATTAATT

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                                                  CTTCAGGCTCCCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAAGCTTCTGTACT 4267
                                                                                                                                                                                              CCATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGA 4147
                                                                                                                                                                                                                                         GTGTTAATATTCCTGCTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGT
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                                                                                                                          AGCTGTCCTCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAG
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                                  CTTCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAAGCTTCTGTACT
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/mol type="genomic DNA"
/db_xref="taxon:9606"
/note="Incyte ID No: 3658034CB1"
239 c 289 g 419 t
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On Aug 1, 2001 this sequence version replaced gi:15021177.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em:, EMBL; Sw:,
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMPORTANT: This sequence is not the entire insert of clone RRP11-53A21 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap.
The true right end of clone RP11-553A21 is at 163577 in this sequence. The true left end of clone RP11-525G3 is at 88067 is sequence. The true right end of clone RP3-397H23 is at 2000 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RP11-553A21 is from the library RPCI-11.2 constructed by the of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 163577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (31-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL590428 AC026605
AL590428.7 GI:15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VECTOR: pBACe3.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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1166. .1384
/note="L1MC5 repeat: matches 7317. .7536 of consensus"
                                                                                                                                                                                                              434. .743
                                                                                                                                                                                                                                                                       285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                    744. .919
                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
[mol_type="genomic DNA"]
                                                                                                                      note="AluJb repeat:
                                                                                                                                                                                  'note="AluY repeat: matches 1.
                                                                                                                                                                                                                                         note="AluJb repeat: matches 1.
                                                                                                                                                                                                                                                                                                                              clone="RP11-553A21"
                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:9606"
chromosome="6"
                                                            note="L2 repeat: matches 2626. .2708 of consensus"
                                                                                                                                                                                                                                                                                                   clone_lib="RPCI-11.2"
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                                                                                                                         matches 119.
                                                                                                                                                                                  .311 of consensus"
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/note="AluSx repeat: matches 1. .306 of consensus"
1691. .1759
                                                     note="AluY repeat: matches 1. .288 of consensus"
                                                                        note="MER39 repeat:
3926. .14215
                                                                                                                                                  note="AluSq repeat: matches 1.
3637. .13697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293. .9415
note="MER33 repeat: matches 1.
516. .9647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="L1MC3 repeat: matches 6740. .7398 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="MLT2FB repeat: matches 1. .403 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluJo repeat: matches 3.
                                                                                                                            note="AluS repeat: matches 1. .63 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               387. 8168
note="AluSq repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179. .8975
Note="MER33 repeat: matches 129. .323 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="AluSx repeat: matches 1.
                                                                                                                                                                                                                                                                                             ote="L2 repeat: matches 2588. .2707 of consensus"
561. .12844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ote="33 copies 2 mer tc 89% conserved
                                                                                                                                                                                     ote="FLAM_C repeat: matches 1.
451. .13636
                                                                                                                                                                                                                     ote="AluSp repeat:
294. .13417
                                                                                                                                                                                                                                                                                                                                                                                    .22. .11798

ote="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ote="MIR repeat: matches 106.

    .8729
    te="AluSq repeat: matches 1. .302 of consensus"

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05. .10048
                                                                                                                                                                                                                                                                                                                              e="SVA repeat: matches 519. .1386 of consensus"
18. .12152
                                                                                                                                                                                                                                                                                                                                                                                                                                  e="SVA repeat: matches 3.
                                                                                                                                                                                                                                                                                                                                                                dence=not_experimental 6. .11951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="22 copies 2 mer tt 79% conserved"
                      e="MER39 repeat: matches 148. .543 of consensus"
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                                                                                                                                                                                                                                                                         e="AluSx repeat: matches 3.
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                                                                                            15.
                                                                                                                                                                                                                                                                                                                                                                                                                                    .954 of consensus"
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ATTCAAACAGACAAGGCCTTATACAAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACA 456 GAGATTTTATTCTCTAATAGTACCCGCTTATCATTTGAGACCAAGAGAATATCTGTCTTC GAGATTTTATTCTCTAATAGTACCCGCTTATCATTTGAGACCAAGAGAATATCTGTCTTC CTACCTCTGAACAGTGCAGATGAGATTTATGAGCTACGTGTAACCGGACGTACCCAGGAT

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Matches 232;
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                                                       27866. .27943
/note="MDT1J repeat: matches 410. .492 of consensus"
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14832. .15863
                                                                                                                                                            5614. .25730
note="FLAM_C
                                                                                               note="L1M4 repeat: matches 4499. .4833 of consensus"
                                                                                                                                                                                                5494. .25519
note="13 cop:
                                                                                                                                note="AluJb repeat: matches 7. .311 of consensus"
                                                                                                                                                                                                                                                                                                                                                    note="AluSx repeat: matches 142. .309 of consensus" 1243. .24416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10te="AluSx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="AluSg/x repeat: matches 87. .262 of consensus"
1895. .23001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0319. .20442
10te="AluJo/FRAM repeat: matches 179. .305 of consensus"
                                                                                                                                                                                                                                ote="AluSx repeat: matches 1. .299 of consensus"
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                                                                                                                                                                                                                                                                                                  ote="AluSx repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                     ote="AluSg
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             5.4%; Score 232; DB 9;
100.0%; Pred. No. 6.9e-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e="AluSq/x repeat: matches 12. .112 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e="L2 repeat: matches 2636. .2734 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .1651
                                                                                                                                                                                                copies 2 mer at 100% conserved"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat: matches 14.
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                                                                                                                                                               repeat: matches 2.
                                                                                                                                                                                                                                                                  repeat: matches 1. .363 of consensus"
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Mismatches
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ALIGNMENTS

standard; DNA; 4369 BP.

Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; gene; ds.

Location/Qualifiers 26..4312 /product= "Human r1520 protein #1" /transl_except= (pos:2132..2134, aa:Xaa) /note= "Xaa corresponds to Ser, Tyr" /*tag= a

Result No.

24-APR-2002; 2002WO-CA00560

24-APR-2001; 2001US-285713P 14-FEB-2002; 2002US-356163P

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Query Match
Best Local Similarity
Matches 4283; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta useful for negatively modulating TGF-beta activity, and thus for
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                 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG
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  CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG
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Db 3746 AATGTTGTATATATGGAGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAAT 3805 Qy 3781 CAAGAAGCCTTTGATTTAGATGTGCTGTAAAAGAAAAAAAA		3386 3386 3421 3446 3506	3206 AAGTATCAGCCTAACATTATACTCTAGCCTTATGCAGTAGCAGAACAAGAAGGGGGGGG	3026 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAAGGACAT 3061 CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGGTGATTCATAGTGAGCTTCAAGGT	Qy 2821 AAAAAGAACAGTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT 2880

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                                                                                                                    New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, throm thrombocytopenia, autoimmune diseases, or organ or bone marrow
                                                                                                                                                                                                                            WPI; 2002-713450/77.
P-PSDB; ABB82165.
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     The invention relates to isolated nucleic acid molecules encoding CD109
                                                  Claim 1; Fig la; 156pp; English.
                                                                                                                                                                                                                                                                                                   Schuh A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC polypeptides. These nucleic acid molecules include the human cDNA CS sequences comprising CD109 K1, CD109 K1-17, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CG family of thioester-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CG for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes and of the complement system, quantitative or qualitative abnormalities CC activation, increased or impaired or impaired platelet aggregation and CC activation, increased or impaired activation or the coagulation and or correct or also useful for treating cardiovascular disorders, stroke, myocardial infarction, thrombosis, embolism, peripheral vascular disease, CC infarction, thrombosis, embolism, peripheral vascular disease, organ CC transplantation, or bone marrow transplantation. The CD109 nucleic acids or their antisense nucleotide sequence are useful in gene therapy for CC treating these conditions. The present sequence represents the human consider conditions. The present sequence represents the human consider the present sequence represents the human consider the present sequence represents the human considered to the present sequence represents the human considered conditions.
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  GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT
                                                                                                        TCACAACAAAGTGATCTTGGAGTCATTTCCCAAAACTTTTCAGCTATCTTCCCATCCAATA
                                                                                                                                                                                                                                                                                                      AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG
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                                                                              TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCCATCCAATA
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Pred. No. 0;
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2821 AAAAGAACTGACGACTAATTTGAAAGAAAGCTCTTTCATTTATGAGGCAAGGT 2880	701 1919919ACASSACAISA AAAII119C CCAAAIAIIAAAII119ACI CAACI 19ACI	641 AGTTTCTCATTTCCTCCTAATACAGTGACTGGCAGTGAAAGGTTCAGATCACTGCAATT	581 TCACAATCCATCTTATTAGACTTGACTAGACATAGGCTACAGAGTACCCTGAAAACTTTG 693 TCACAATCCATCTTATTAGACTTGACAGATAGGCTACAGAGTACCCTGAAAACTTTG	521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT	61 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT 	01 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGGCAACTGTTCTTTTT 13 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT	341 AGGTRATCATTGAGAAAAGTGACAAATTGATATCTAATGACTTCAAGTGAAATAAAT	281 GGIGAAGAATITIGCITITGGAAATAACTAITATTCAATTATTTGAAAGATGCCACTGAGGTT [221 GAGCTCCAAGCCTTCCAACCATTITTCATTTTTTTGAATCTTCCCTACTCTGTTATCAGA [161 GTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTACTACTACTCCAGTG	101 ATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG	041 GTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGGTTTGGCTAGACACCAAC	981 GCTGRGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG	21 TTGACAGATGCAGACCTCACGAAGGATTATATGATGATGATGATATTGATGATGATATTGATGA	973 TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA	913 GCCTCTAATGATATACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA	1801 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA 1860	

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TTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTG
                                                                                              GTGTGTACAAGCTTTTCGGGCCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA
                                                                                                                                                                                   TTTGATTTAGATGTTGCTGTAAAAGAAAATAAAGATGATCTCAATCATGTGGATTTGAAT
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WO200285942-A2

24-APR-2002; 2002WO-CA00560

24-APR-2001; 2001US-285713P. 14-FEB-2002; 2002US-356163P.

(UYMC-) UNIV MCGILL.

Philip P, Tam ₽,

WPI; 2003-093100/08

Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta useful for negatively modulating TGF-beta activity, and thus for treating cancer

Disclosure; Fig 17; 127pp; English.

The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability

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Matches 4286
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                    ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG
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                         TTGACAGATGCAAACCTCACGAAGGATTATATTGATGATGTGTTTATGACAATGCAGAATAT
                                                   GCCTCTAATGATATTACAATGGAAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA
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            The invention relates to isolated nucleic acid molecules encoding CD109
C polypeptides. These nucleic acid molecules include the human cDNA
C sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants.
CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5
CE family of thioester-containing proteins. The CD109 polypeptides can be
cexpressed by standard recombinant methodology. The CD109 mucleic acid,
CC CD109 polypeptide or its minetic, or the anti-CD109 antibody is useful
CC for treating or detecting a disease or disorder, e.g. conditions
CC associated with endothelial activation, platelet activation, activation
CC of the complement system, quantitative or qualitative abnormalities
CC and of the complement system, quantitative or qualitative abnormalities
CC of platelet function, increased or impaired platelet aggregation and/or
CC fibrinolytic systems, or impaired activation of the coagulation and/or
CC fibrinolytic systems, or impaired or increased immune activation. These
CC are also useful for treating cardiovascular disorders, stroke, myocardial
CC infarction, thrombosis, embolism, peripheral vascular disease, organic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CD109; alpha2 macroglobulin; thioester; cerebroprotective; c: immunosuppressive; haemostatic; anticoagulant; thrombolytic; cardiovascular; vasotropic; gene therapy; CD109 KI-H7; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
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      thrombocytopenia, thrombocythemia,
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Mismatches

Indels Length other;

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Gaps

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Score 4223.4; Pred. No. 0;

Sequence

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BP;

1696 A; 1173 C;

1241 G;

1772 T; 1 DB 2; 25;

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                                                   The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                              Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; GPI-anchored TGF-betal binding protein; r150 protein; can glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                Claim 7; Page 100-103; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Philip A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2001;
14-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human r150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-093100/08
DB; AAE32013.
                                                                                                                                                                                                                                                                                                                                                                                                            cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGAACTTTGGCTGTGA 4287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAAGCTTCTGTACTTT 4269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGTCCTCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT
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2002US-356163P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002WO-CA00560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Human r1520 protein #2"
/transl_except= (pos:2219..2221, aa:/note= "Xaa corresponds to Ser, Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA; 5883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               aa:Xaa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4432
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901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780	541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600	361 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA	293 ĠAĠĊTĠĊŦĊAĀĠĊĀŢĊĀĀĀĊŢĊĀĊŦĠŢĊŢĊŢĠŢĊĊŢĠĠĀĀĠĠĀĠĀĠĠĀĠŢĊŢŢ 352 241 GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 300	1 ATGCAGGGCCCACCGCTCCTGACCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG 60
Oy 1981 GCTGAGAGGTTTATGAGGAGAAATGAAGGACATATTGTAGATATTCATGACTTTTTTTT		1733 GAAATTATAAGTGATATTACAAAGTGGAAAATTCCTGGTGTGGAAAAGTGGAACTTCTAAAAATTAAGAGAAATTCCTGGTGTTCAAAAGTGAAAGTGAAAGTGAAAGTGAAAGTGAAAGTTGAAAGTTGAAAGTTCTCTGTGGTGTTTTTAAAAATTAAGATTAAAGTGAAAGTGAAAGTTGAAAGTCTAAGAATTCTCTGTGGTTTTTAAAAATTAAGAAAAGTGAAAAGTTGAAAAAGTGAAAAGTTGAATGAATTAAGAATTAAGAATTGAATTGTAAGATTGTAAGATTGTAAGAATTGTAAAAAGTGTGAAAAAGTGTGAAAAAGTGTAAAAAGTGTAAAAAGTGTAAAAAGTGTAAAAAGTGTAAAAAGTGTAAAAAA	1553 TGGC 1501 GTAT 1613 GTAT 1561 CCAG 1673 CCAG	1321 CTAC 1433 CTAC 1381 AAGT 1493 AAGT 1441 TCGC	Qy 1081 AAGCCATCTCCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC

8	B 8	D Qy	B Q	유 성	B &	B 8	99 99	B 8	용 성	dg Qy	B 8	Db Qy	B 8	g &	문 성	망왕	B 8	Db
3241 AGAGGAATTTCAGACAATTATACTCTAGCCCCTTATAACTTATGCATTGTCATCAGTGGGG 3300	3181 AAGTATCAGCCTAACATTGATGTGCAAGAGTCTATCCATTTTTTGGAGTCTGAATTCAGT 3240	3121 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCCCTGGGATATAGA 3180 	3061 CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT 3120 	3001 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3060 	2941 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTTTTTTT	2881 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGGAATTAT 2940	2821 AAAAAGAAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT 2880 	2761 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATCTGACT 2820	2701 GARGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTCGGATGCCTTATGGC 2760	2641 AGTITICICATITICCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT 2700 	2581 TCACAATCCATCTTATTAGACTTGACTACAATAGGCTACAGAGTACCCTGAAAACTTTG 2640	2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT 2580	2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCAACAGCTCTTTCACCCACT 2520	2401 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT 2460	2341 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT	2281 GGTGAAGAATTTGCTTTGGAAATAACTATATTTCAATTATTTGAAAGATGCCACTGAGGTT 2340	2221 GAGCTCCAAGCCTTCCAACCATTTTTCAATTTTTTGAATCTTCCCTACTCTGTTATCAGA 2280	
₽ Q	Db	Q B 1	\$ B &	D	D 5	, p &	Db Qy	Db	D 5	o do Oy	Db V9	Q dd) D Q	ρb	Оу	Db	Db 49	Db
4270 ATGGAACTTTGGCTGTGA 4287 		TCAGGCTCCCATCACCTCTCAGTCATTTTATTTTCTGTTTCAAGCTTCTGTACTTT	4090 ATAGTIGAATTACTATGAGCCAAGGAGACAGGCGGTGAGAGGTTACAACTCTGAAGGTGAAG 4149 4090 ATAGTIGAATTACTATGAGCCAAGGAGACAGGCGGTGAGAGAGTTACAACTCTGAAGTGAAG 4149 4090 ATAGTIGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGGTTACAACTCTGAAGTGAAG 4312 4253 ATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAGGTGAAG 4312 4150 CTGTCCTCCTGTGAACCTTTTGGAGGTGATGGAGGTGAGGATGGAGGTGAGATGGAAGGT	GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC	GAATATGATCATGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGT	TARGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGC	3850 GTGTGTACAACCTTTTCGGGCCCGGGTAGGACTGGCATGGCTCTTATGGAAGTTAACCTA 3909	3790 TTTGATTTAGATGTTGCTGTAAAAGAAATAAAGATGATCTCAATCATGTGGATTTGAAT 3849		ATGGCAGTTAATATTTCCGCAAATGGTTTTGGATTTGCTATTTCTCAGCTCAATGTTGTA	3652	3601 GAAAGGACAAATATCCAAGTGACCGTGACGGGCCTAACTCCACGAGTCCT 3651	541 ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTGCAGCCCTAATGAATACA	3481 GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAGAATAGCTTGGGTGGTTTTGCATCT 3540		3361 ATGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGGGCAGCCAGGCTCCCTG 3420	301 AGICCTAAAGCGAAGGATTTGAATATGCTGACTTGGAGGAGAACAAGAAGGTGGC 	

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                                                                                                                                  The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioester-containing proteins. The CD109 polypeptides can be CC expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC associated with endothelial activation, platelet activation, activation of the complement system, quantitative or qualitative abnormalities CC associated with endothelial activation of platelet aggregation and cf the complement system, quantitative or qualitative abnormalities CC and of the complement system, quantitative or qualitative abnormalities CC inflation, increased or impaired activation of Tlymphocytes CC are also useful for treating cardiovascular disorders, stroke, myocardial CC inflation, thrombosis, embolism, peripheral vascular disease, CC are also useful for treating cardiovascular disorders, stroke, myocardial CC inflation, or bone marrow transplantation. The CD109 mucleic acids CC or their antisense nucleotide sequence are useful in gene therapy for CC transplantation, or bone marrow transplantation. The CD109 mucleic acids CC or their antisense nucleotide sequence are useful in gene therapy for CC cutos CC or the present sequence represents the human CC cd or the complaint cDNA sequence.
Query Match
Best Local Similarity
Matches 4285; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
                                                                                  Sequence 4761 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schuh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ79965 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SCHU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUTH/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCHUH A.
SUTHERLAND R D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB82166
                                                                                                                           variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sutherland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ፫
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                         cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "CD109 K1 variant"
                                                                                1419 A; 913 C; 1016 G; 1413 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry
                   98.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4761
Score 4222.8;
Pred. No. 0;
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                       AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG
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941 GACCCTTCT9GGAGCACTTQGTTGTCAGCTTTTTTTTAAATGTTTCCTTGAAGCCGAT 053 GACCCTTCTGGAGCACTTGGTTGTCAGCTTTTGTTTTAAAATGTTTCCTTGAAGCCGAT) p 5	1861 TATTATTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1920 	유 성
TACCAGAGAGACTICTCTATCAGAGGGAAGATGGCTCTTTCGGGATTAT) B &	1801 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA 1860 	용 성
AAAAGAACAACTGACAGAFAATTGAAAGAAAAGCTCTTCATTTATGAGGCAAGGT	. B &	1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT 1800	음 성
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GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAATCATATT	S B 8	1441 TCGCCTTTTGAGTTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAAGCTATATGGTA 1500 	용 성
CCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGGTCACAGGCTCTTTCACCCACT) p &	1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGAGGAAAATATAAAGGTGGGA 1440 	유 성
CCACAGGCCACCAGGAGACCCTTCTGGTTCCAGTGAGATGGGGGGAGACTGTTCTTTTT	2 & &	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT 1380 	유 성
ANGGIAATCAITGAGAAAAGIGACAAATTIGAIAITCIAAIGACTTCAAGIGAAATAAAT	} B &	1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1320 	음 성
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                                                             TCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAAGCTTCTGTACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Fig 2b;
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/product= "CD109 K1-H7 variant"
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The invention relates to isolated nucleic acid molecules encoding CD109 CD polypeptides. These nucleic acid molecules include the human cDNA CD sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 family of thioester-containing proteins The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its minetic, or the anti-CD109 antibody is useful CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of Tlymphocytes and of the complement system, quantitative or qualitative abnormalities CC associated tinuction, increased or impaired activation of Tlymphocytes activation, increased or impaired platelet aggregation and CC of platelet function, increased or impaired application and contivation of the coagulation and contivation contivation continued association. These care also useful for treating cardiovascular disease, myocardial continued c or their antisense nucleotide sequence treating these conditions. The present CD109 K1-H7 variant cDNA sequence. are useful in gene therapy for sequence represents the human

BP; 1708 A; 1174 C; 1241 G; 1772 T; 0 other,

Query Match
Best Local Similarity
Matches 4285; Conserv Conservative 98.5%; Score 4222.8; Pred. No. 0; 0; Mismatches 0, В 24; Length 51; 5895; Gaps

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2101 ATGGGTTACAGAATTTACCAAGAATTTGAAGTACTGTACCATCATACACTTCTTGG 2160 2101	GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAAC	1981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG 2040	1921 TTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTTATGACAATGCAGAATAT 1980		GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA	1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT 1800 	1681 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG 1740 	1621 GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAAG 1680 	1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG 1620 	1501 GTATICCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTTAACA 1560 	1441 TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA 1500 	1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA 1440 	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT 1380 	1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1320 	1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	1141 ACTCTTGAAGAAAGAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 1200 	1081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC

2221 GACTICAACCUTTCTAACAACTITTTOATTTTTTOATTCTTCAACTAACACTACTCCTAACTTTTTTCAACTACT
B
3353 AAAGAANTTCAAGACANATRACCTTTGATATACCTTATACCTTATACCATAGCCCAAACACAAACATGCCCTAAAACATGCCAAACACAACACAACACTGCCCTAAAACAAAC

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RESULT 8
ALL49815
ID ALL49815
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                                                                                                                                                             The present invention relates to a sequence capable off binding specifically to a CD109 nucleic acid which has a single nucleotide polymorphism that distinguishes the Gova and Govb alleles. Detection of the Gov genotype is useful for detecting whether the subject has or is at risk of a blood disease, disorder or abnormal physical state, such as bleeding, or increased risk of bleeding, due to alloimmune destruction of blood platelets, e.g., post-transfusion purpura, post-transfusion platelet refractoriness or neonatal alloimmune thrombocytopenia. The nucleic acid and polypeptide are useful for Gov genotyping or phenotyping individuals. The present sequence is the Gova coding sequence.
                                                                                                                                                                                                                                                                                                                                          New isolated oligonucleotide binding to a region of CD109 nucleic acid having a single nucleotide polymorphism that distinguishes a Gova and/or Govb allele, useful for treating blood disorders e.g. alloimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-MAR-2001; 2001US-273941P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; platelet alloantigen; Gova; Govb; single nucleotide polymorphism; SNP; biallelic; bleeding disorder; post-transfusion purpura; post-transfusion platelet refractoriness; haemostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; platelet alloantigen; Gova; SNP; biallelic; bleeding disorder;
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                                                                                                                                                                                                                                                                                                         Claim 6;
                                                                                                                                                                                                                                                                                                                               thrombocytopenia
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                                                                                                    Local Similarity
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DB; AAO19372.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alloimmune thrombocytopenia; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated oligonucleotide binding to a region of CD109 nucleic acid having a single nucleotide polymorphism that distinguishes a Gova and/or Govb allele, useful for treating blood disorders e.g. alloimmune thrombocytopenia
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT
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nilarity 98.8%;
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Pred. No. 0;
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dg VQ	D Qy	β &	g gy	Qy Db	D Qy	Qy Db	Qy Db	Qy db	95 85	B &	η δ	dg Qy	Db Qy	Qy Db	Qy db	Qy Db	. Ag	рb
2341 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT	2281 GGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTGAAAGATGCCACTGAGGTT 2340 			TACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG 2 	2041 GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAAC 2100 	1981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG 2040	1921 TIGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTTATGACAATGCAGAATAT 1980 	1861 TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1920	1801 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA 1860 	1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT 1800 		1621 GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAAG 1680 	1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG 1620	1501 GTATICCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACA 1560 	1441 TCGCCTTTTGAGTTGGTGGTTAGTGGCAACAAACGATTGAAGGAGTTAAGCTATATGGTA 1500 	1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA 1440 	1321 CTACAGTIGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCAIGGCAGTTCATAGTCIGTTT 1380	ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG

3421 GATATTGAAGTTGCAGCCTATGCACTGCTCTCACACTTCTTACAATTTCAGACTTCTGAG 3
3361 ATGCAAITCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGGCAGCCACGCTCCC
3301 AGTCCTAAAGCGAAGGAAGCTTTGAATATGCTGACTTGGAGAGCAGAACAAGAAGG
3241 AGAGGAATTTCAGACAATTATACTCTAGCCCTTATAACTTATGCATTGTCATCAGTGGGG
181 AAGTATCAGC
3121 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCCTCGGGATATAGA
190
3001 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT
2941 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGA
2881 TACCAGAGAGACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGGAATTAT
2821 AAAAAGAAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGG:
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2641 AGTTTCTCATTTCCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT
2581 TCACAATCCATCTTATTAGACTTGACAATAGGCTACAGAGTACCCTGAAAACTTTG
2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATA
2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT
2401 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT

Hydrophobic domain protein cDNA HP02837 isolated from HT-1080 cells. Human; secreted protein; membrane protein; hydrophobic domain; proliferation control; differentiation induction; material transport;

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ATGGAACTTTGGCTG 4284 ATGGAACTTTGGCTG 4335	TCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAAGCTTCTGTACTTT 4269	CTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT 42	ATAGTGGATTACTATGAGCCAAGGAGACAGGCGGTGAGAAGTTACAACTCTGAAGTGAAG 4149 	GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC 4089 	GAATATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGT 4029 	TTAAGTGGCTTTATGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAGTG 3969 	GTGTGTACAAGCTTTTCGGGCCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA 3909 	TTTGATTTAGATGTTGCTGTAAAAGAAAATAAAGATGATCTCAATCATGTGGATTTGAAT 3849 	TATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAATCAAGAAGCC 3789 	ATGGCAGTTAATATTTCCGCAAATGGTTTTGGATTTGCTATTTGTCAGCTCAATGTTGTA 3729 	CTTGCTGTGGTACAGCCA 3669	GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCT 3651 	ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA 3600	TCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT 354

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Best Local :
                                                                                                                                                                                                                                                                                                         secretory proteins play important roles in the proliferation control, the differentiation induction, the material transport and the biophylaxis of cells. Membrane proteins have important roles as signal receptors, ion channels and transporters. The present sequence is the coding sequence for a human protein which has at least one hydrophobic domain. The protein encoded by the present sequence may be a secretory or a membrane protein. The encoded protein may have cytokine and cell proliferation/differentiation activity, immune stimulating or suppressing activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, tissue growth activity, haematopoiesis activity, activity and thrombolytic activity, anti-inflammatory activity and tumour inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's disease, and cancer via gene therapy.
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P-PSDB;
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16-MAR-1999;
27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -
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                                                                                                                                                                                                                                                                                     Sequence 4473 BP; 1328 A; 867 C;
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   GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG
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98.7%;
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Pred. No. 0;
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proliferation control; differentiation induction; mechanical proliferation control; differentiation induction; mechanical proliferation control; identification; chemotactic; chemokinetic; immunosuppressant; haematopoiesis regulator; chemotactic; chemokinetic; haematopoietic; anti-inflammatory; tumour inhibition; anti-inflammatory; tumour inhibition; anti-inflammatory; tumour inhibition; anti-inflammatory; tumour inhibition;
                                                                                     Human; secreted protein;
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                                                                                                                    domain protein cDNA HP02837 isolated from HT-1080
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98JP-0364315.
99JP-0069811.
99JP-0119299.
99JP-0138169.
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Proteins comprising hydrophobic regions, such as secretory and membrane proteins, useful in research and diagnostics and having various activities e.g. immunomodulatory, antiinflammatory, chemokinetic, hemostatic, thrombolytic -

Claim 3; Page 244-246; 410pp; English.

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CC differentiation induction, the material transport and the biophylaxis of CC cells. Membrane proteins have important roles as signal receptors, ion CC channels and transporters. The present sequence is the coding sequence CC protein encoded by the present sequence may be a secretory or a membrane CC protein. The encoded protein may have cytokine and cell CC proteiration/differentiation activity, immune stimulating or suppressing CC activity, haematopoiesis activity, tissue growth activity, haemostatic CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, anti-inflammatory activity and tumour CC inhibition activity. The present sequence could therefore be used for treatment of autoimmune disease, Alzheimer's disease, Parkinson's CC disease, and cancer via gene therapy.

4335 BP; 1295 A; 838 C; 922 G; 1280 T; 0 other;

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AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCTCTGCGTGTGCACCGCCGCGCTG ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCGCTG GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGGTCCTGGAAGCAGAAGGAGTCTTT GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA 98.4**%**; 98.7**%**; Score 4216.6; Pred. No. 0; 0; Mismatches <u>,</u> 멂 4 21; Length Indels 4335; 51; Gaps 360 300 300 240 180 180 120 120 60 60

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1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAGAGATGAAAATATAAAGGTGGGA 1440	1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT 1380	1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1320	1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	1141 ACTCTTGAAGAAAGAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 1200	1081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC	1021 AATGTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTG 1080	961 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020 	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGAG	781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAA	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780	661 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT 720	601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAATGACCAGACATATTATCAATCA	541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600	481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540	421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC 480	361 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA	
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2461 CCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGGTCACAGCTCTTCACCCACT 2520 2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT 2520	#101 GCCACAGGCCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGGAACTGTTCTTTT 24 401 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGGAACTGTTCTTTTT 24	341 ANGGIAATKATIGKGAAANGTGAKAAATTIGATATTCIAATGAKTTCAAGTGAAATAAAT	281 GGTGAAGAATTIGCTTIGGAAATAACTATTATTCAATTATTGAAAGATGCCACTGAGGTT	221 GAGCTCCAAGCCTTCCAACCATTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGA 1	16.1 GIGGCTACIGGITITGIGATCICIGAGGACCIGGGICITGGACIAACAACTACICCAGIG 2	101 ATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG 2 101 ATGGGTTACCAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG 2 101 ATGGGTTCCAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG 2	041 GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAAC 	961 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG 981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTTG	TIGACNATIGCAAACCICACGAAGGAITAIATIGAIGGIGTITAIAIGACAAIGCAGAAIATITIIIIIIIIII	TATIATITAGGCATGTTCAGAATTCTTTTGCAGTCTTTCAGGATGTGGACTCTGGGTA 1 TATTATTTAGGCATGTTCAGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1	GCTTTAATGATTACAATGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA	ACACAGCCIGACICCALAGIIIGGGAIIGIAGCIGIIGACAAAAGIGIGAAICIGAIGAAGIAGAAGIGIGAAICIGAIGAAGIAGAAGIGIGAAGAAGAGAGAG	CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTGTGTG	GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAAAATTAAGATTAAAAATTAAGATTAAAAATTAAAAATTAAAAATTAAAAAA	CCASAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG	COALLANGEMENT OF TOWN OF THE STATE OF THE ST	TOGGCCTTTTGAGTTGGTTGGTTGGTGGCCAAACGATTGAAGGAGTTAAGCTATATGGTA 15	

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                  GAATATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGT
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standard; DNA;

24-MAR-2003 (first entry)

Human blood cell surface antigen, CD109 encoding DNA

Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; blood cell syrface antigen; CD109; gene; ds.

sapiens

Location/Qualifiers
1..4146
/*tag= a
/product= "Human CD10"

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"Human CD109

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-betal binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human blood cell surface antigen, CD109 encoding DNA. CD109 is a variant of r150 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; Page 109-112; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
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14-FEB-2002;
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                                                                                           TTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCAAACAGACAAGGCCTTATACAAG
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                                                                             TTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCAAACAGACAAGGCCTTATACAAG
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2002US-356163P.
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/note= "Xaa corresponds to Ser, Tyr; No start
and stop codon"
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99.9%;
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Pred. No. 0;
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                                     AAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGAGTGAAAAAT
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2524 TCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATATTCA 2583	404 ACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTTCCC	84 GAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTGAAAGATGCCACTGAGGTTAAG 2	4 4 4	44 AGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACGACATG 210	1924 ACAGATGCAAACCTCACGAAGGATTATATTTGATGGTGTTTATGACAATGCAGAATATGCT 1983	1804 TCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGATAT 1863	1501 GAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTAAAGATGAAGATGAAGCTA 1560 1624 ATTATAAGTGATGTTCTAAAAATTCCTGGTTCAGCTTGTTTTTAAAATAAGATAAAGCTA 1683
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                                  AATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTGAAA
                                                                                                            TCAGAATATGTATTACCAAAATTTGAAGTGACTTTTGCAGACACCATTATATTGTTCTATG
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98.7%;
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Pred. No. 0;
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Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for

The invention relates to novel transforming growth factor (TGF)-betal binding reagent which comprises a glycosylphosphatidyl inositol (GPI)-anchored TGF-beta binding protein referred to as r150 which acts as an accessory receptor of TGF-beta. The invention is used for negatively modulating TGF-beta activity, and thus for treating conditions characterised by overproduction of TGF-beta, such as cancer. Antisense molecules of the invention are used for increasing TGF-beta availability and increase graft success. The present sequence is human r150 protein according man

GTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGGCCCCGGAGGAAAAT GTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGGCCCCGGAGGAAAT DB 25; Indels Length 51; 4197; Gaps 123 60

1864 TATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTATTG 1923	TCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGAGATAT	CAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAATGCC	TATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTGACA	ATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTAAAAATAAGATAAAGCTA	1564 GAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGATTATATTTGAAGATGATGGGGAA 1623 	TCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTCTTTAACACCA		TCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGATCG 	1324 CAGTIGAAGGCCTATITCCTTGGTAAGAAGTAGCATGGCAGTTCATAGTCTGTTTAAG 1383 	GTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAGCTA 	TGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT	1144 CTTGAAGAAAGAAGAATAATGTAGTCATAACAGTGACACAGAGAAAACTATACTGAGTAC 1203 	1084 CCATCTCTAACTTCACAGCCACTGTGAAGGTAACTGGTGCTGATGGCAACCAAC	1024 GTGTTCTTCAAGCAACATGATTACATCATTGAGTTTTTTGATTATACTACTGTCTTTGAAG 1083 	964 GAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACTAAT 1023 	904 GTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT	721 GGAGACGTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAA	
B 9	Db Qy	Db Qy	Db Qy	Qy db	D Q	D Q	B &	g Qy	₽ Q	dg Qy	D Q	B &	da Vo	dg VQ	dg Vy	B &	ט אָט ט	-
2944 CCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGATCCT 3003		2824 AAGAAACAACTGACAGATAATTTGAAAGAAAAGCTCTTTCATTTATGAGGCAAGGTTAC 2883 		2704 GATGITCTIGGICCTICCATCAATGGCTTAGCCTCATIGATICGGATGCCTTAIGGCIGI 2763	2644 TTCTCATTTCCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATTGGA 2703	2584 CAATCCATCTTATTAGACTTGACTGACAATAGGCTACAGAGTACCCTGAAAACTTTGAGT 2643 	2524 TCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATATTCA 2583 	2464 ATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACTGCT 2523	2404 ACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTCCC 2463	2344 GTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT	2284 GAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTGAAAGATGCCACTGAGGTTAAG 2343 	2224 CTCCAAGCCTTCCAACCATTTTTCATTTTTTGAATCTTCCCTACTCTCTTATCAGAGGT 2283	GCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACAACTACTCCAGTGGAG 	GGTTACAGGATTFACCAAGAATTGAAGTAACTGTACCTGATTCTATCACTTCTTGGGTG	AGCAGTCCACATGTCCGAAAGCATTTTCCAGAGCTTTGGATTTGGCTAGACACCAACATG	GNONGGILLALGENGGANANIGANGSANALALIGANGALALICALGANGLILLICILLOSGI 	TATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTATTG ACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTATGACAATGCAGAATATGCT	

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                    TATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGTGTT
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CC The invention relates to isolated nucleic acid molecules encoding CD109 CC polypeptides. These nucleic acid molecules include the human cDNA CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the complement system, quantitative or qualitative abnormalities CC and of the complement system, quantitative or qualitative abnormalities CC of platelet function, increased or impaired platelet aggregation and CC activation, increased or impaired activation of the coagulation or fibral activation of the coagulation and or cfibrinolytic systems, or impaired activation of the coagulation and/or CC complement system, or impaired activation activation. These care also useful for treating cardiovascular disorders, stroke, myocardial cc infarction, thrombosis, embolism, peripheral vascular disease,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human; cardiovascular; vasotropic; gene therapy; CD109 K15; gene; ss.
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Matches 3188; Conserv
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CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT
                           CAGAAATCCAACGGTGAATTTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT
                                                                                                             CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3060
                                                                                                                                                                                                                  GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT 3000
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particularly for treating strokes, myocardial infarctions, thrombocytopenia, autoimmune diseases, or organ or bone marrow New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis,

P-PSDB; ABB82170

2002-713450/77.

Claim 1; Fig 4b; 156pp; English.

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The invention relates to isolated nucleic acid molecules encoding CD109
CC polypeptides. These nucleic acid molecules include the human cDNA
CC sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants.
CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5
CC family of thioester-containing proteins. The CD109 polypeptides can be
ce expressed by standard recombinant methodology. The CD109 nucleic acid,
CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
CC for treating or detecting a disease or disorder, e.g. conditions
CC associated with endothelial activation, platelet activation, activation
CC associated with endothelial activation, platelet activation of Tlymphocytes
CC and of the complement system, quantitative or qualitative abnormalities
CC and of the complement system, quantitative or qualitative abnormalities
CC of platelet function, increased or impaired platelet aggregation and/or
CC fibrinolytic systems, or impaired or increased immune activation and/or
CC are also useful for treating cardiovascular disorders, stroke, myocardial
CC infarction, thrombosis, embolism, peripheral vascular disease, thrombocytopenia, thrombocythemia, autoimmune diseases, organ transplantation, or bone marrow transplantation. The CD109 nuc or their antisense nucleotide sequence are useful in gene them

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	901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGAICTATCTTCCCCTGGACCA 960	953 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 1012	ACAAAAAC	781 AAAGGAGACGTTACACTTTTACCTTTTATCCTTTTGGGGAAAGAAA	721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780	661 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT 720 	601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAATGACCAGACATATTATCAATCA	541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600 	481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540	421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC 480 	361 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA	301 ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC 360 	241 GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG 300 	181 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT 240	121 AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG 180	61 GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA 120	1 ATGCAGGGCCCACCGCTCCTGACCGCCCACCTCCTGCGTGTGCACCGCCCGC	Query Match 74.3%; Score 3185.8; DB 24; Length 3535; Best Local Similarity 99.9%; Pred. No. 0; Matches 3187; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	treating these conditions. The present sequence represents the human CD109 K15 variant cDNA sequence. Sequence 3535 BP; 1107 A; 676 C; 731 G; 1021 T; 0 other;
	Ş B .	& A	. Q	B :	0 Pb		Q B :	δ β ;	0 v0	Q B 5) B	S B 1	S B &	5 B 8	B &) B 8	ob Q	B &	Qy Ob
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3180	3121 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCCTCCTGGGATATAGA	
3120 3232	061 CAGAAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT 	
3060 3172	3001 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 	
3000 3112	2941 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT	
2940 3052	2881 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGGAATTAT	
2880 2992	2821 AAAAAGAAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGGAAGGT	
2820 2932	2761 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATCTGACT 	
2760 2872	2701 GGAGATGITCTIGGTCCITCCATCAAIGGCTTAGCCTCATTGATTCGGATGCCTTAIGGC	
2700 2812	2641 AGTTTCTCATTTCCTCCTAATACAGTGACTGGCAGTGAAAGAGTTCAGATCACTGCAATT	
26 4 0 2752	2581 TCACAATCCATCTTATTAGACTTGACTGACAATAGGCTACAGAGTACCCTGAAAACTTTG	
2580 2692	2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAATCATAT 	
2520 2632	2461 CCCATCAGGCCAACACCTCGGGAGAAATTCCTATCACAGTCACAGTCACCACCT	
2460 2572	2401 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTTT	
2400 2512	2341 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT	
2340 2452	2281 GGTGAAGAATTIGCTTIGGAAATAACTATATTCAATTATTGAAAGATGCCACTGAGGTT	
2280 2392	2221 GAGCTCCAAGCCTTCCAACCATTTTTCATTTTTTGAATCTTCCCTACTCTGTTATCAGA	
2220 2332	2161 GIGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACAACTACTCCAGTG	
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RESULT 1 AAD49434 CDS Human; GPI-anchored TGF-betal binding protein; r150 protein; cancer; glycosylphosphatidyl inositol; transforming growth factor-betal; therapy; gene; ds. Homo sapiens. Human r150 gene 24-MAR-2003 AAD49434; AAD49434 standard; DNA; 4369 BP (first entry) /transl except= \pvs...-/note= "Xaa corresponds to Ser, product= "Human r1520 protein #1" ocation/Qualifiers except= (pos:2132..2134, aa:Xaa) Xaa corresponds to Ser, Tyr"

24-APR-2001; 2001US-285713P. 14-FEB-2002; 2002US-256163P. 24-APR-2002; 2002WO-CA00560 WO200285942-A2

31-OCT-2002.

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Matches 4283; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively modulating TGF-beta activity, and thus for
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                                                                                                       TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA
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                               New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thrombosis, thrombocytopenia, autoimmune diseases, or organ or bone marrow
Claim 1; Fig
                           transplantation
                                                                                        WPI; 2002-713450/77.
P-PSDB; ABB82165.
                                                                                                                              Schuh A,
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                                                                                                                                                                                                                                                12-SEP 2002.
                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                         cardiovascular; vasotropic; gene therapy; CD109 K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human CD109 K1 protein encoding cDNA.
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CC polypeptides. These nucleic acid molecules include the human cDNA CS sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CC CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 CC family of thioester-containing proteins. The CD109 polypeptides can be CS expressed by standard recombinant methodology. The CD109 nucleic acid, CC CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful CC for treating or detecting a disease or disorder, e.g. conditions CC associated with endothelial activation, platelet activation, activation of the coagulation or fibrinolytic systems, activation of T lymphocytes CC and of the complement system, quantitative or qualitative abnormalities CC of platelet function, increased or impaired platelet aggregation and CC activation, increased or impaired activation of the coagulation and/or CC fibrinolytic systems, or impaired or increased immune activation. These CC are also useful for treating cardiovascular disorders, stroke, myocardial cinfarction, thrombosis, embolism, peripheral vascular disease, organ cc transplantation, or bone marrow transplantation. The CD109 nucleic acids CC or their antisense nucleotide sequence are useful in gene therapy for CC crating these conditions. The present sequence represents the human CC CD109 K1 cDNA sequence.
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Sequence 4761 BP; 1420 A; 912 C; 1016 G; 1413 T; 0 other;

밁 S 밁 Ś 멂 Ś 맑 S 밁 á 밁 8 문 ð 밁 S 밁 Ś 밁 S Ś 밁 Matches 4286; Query Match Best Local Similarity 661 601 653 541 593 481 533 421 473 361 413 301 353 181 233 121 173 241 293 113 61 ۳ GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA ATGCAGGGCCCACCGCTCCTGACCGCCGACCTCCTCTGCGTGTGCACCGCCGCGTG AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCCATCCAATA TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTC ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA ATGCAGGGCCCACCTCCTGACCGCCCCCCCCTCTCTGCGTGCACCGCCGCGCTG Conservative 98.5%; 0 Score 4224.4; Pred. No. 0; Mismatches DB 24; Length 1; Indels CAGATTTTAAGCCTTAC 51; Gaps 540 360 720 772 660 712 600 652 592 480 532 420 472 412 300 352 240 292 180 232 120 172 60

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ALIGNMENTS

TITLE JOURNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX534934	RESULT 1
Cd109 nucleic acid molecules polypeptides and methods of use Patent: WO 02070696-A 1 12-SEP-2002;	Schuh, A. and Sutherland, R.D.	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; .	Homo sapiens	Homo sapiens (human)	•	AX534934.1 GI:25261474	AX534934	ō.	AX534934 4761 bp DNA linear PAT 22-NOV-2002		

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KAEPSEKVSLRISVTQDDSIVGIVAVDKSVNLMVASNDITMENVVHELELYNTGYYLG
MFMNSFAVFQECGLWYLTDANLTKDYIDGVYDNAEYAERFWEENEGHIVDIHDFSLGS
SPHVRKHFPETWIWLDTNMGYRIYQEFEVTVPDSITSWAFTGFVISEDLGLGLTTTPV
ELQAFQPFFIFLMPSEDGATVLFPIRPTHLGEIPITVTALSPTASDAVTQMILVKAEGI
EKSYROGILLDLTDNRLQSTLKTLSFSFPNTVTGSERVQITALSDAVTQMILVKAEGI
EKSYSQSILLDLTDNRLQSTLKTLSFSFPNTVTGSERVQITALGDVLGPSINGLASL
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LALITYALSSVGSPKAKEALMMLTWRAEQEGGMQFWVSSESKLSDSWQPRSLDIEVAA
YALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMMTERTN
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2461 CCCATCAGGCCAACACATCTGGGAGAAATTCCTATCACAGTCACAGCTCTTTCACCCACT 2520	Db Qy		1381 AAGTCTCCTAGTAAGACATACATCCAACTAAAAACAAGAGATGAAAATATAAAGGTGGGA 1440
2401 GCCACAGGCCACCAGCAGACCCTTCTGGTTCCCAGTGAGGATGGGGCAACTGTTCTTTT 2460	ob Oy		1321 CTACAGTTGAAGGCCTATTTCCTTGGTAGTAAAAGTAGCATGGCAGTTCATAGTCTGTTT 1380
2341 AAGGTAATCATTGAGAAAAGTGACAAATTTGATATTCTAATGACTTCAAGTGAAATAAAT	Db Q		1261 ACTGTCCCCCAAAGTGGAACTTTTAAGATTGAATTCCCAATCCTGGAGGATTCCAGTGAG 1320
2281 GGTGAAGAATTTGCTTTGGAAATAACTATATTCAATTATTTGAAAGATGCCACTGAGGTT 2340 	B &		1201 TACTGGAGCGGATCTAACAGTGGAAATCAGAAAATGGAAGCTGTTCAGAAAATAAAT
2221 GAGCTCCAAGCCTTCCAACCÄTTTTTCATTTTTGAATCTTCCCTACTCTGTTATCAGA 2280	p &		1141 ACTCTTGAAGAAAGAAATAATGTAGTCATAACAGTGACACAGAGAAACTATACTGAG 1200
2161 GTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACAACTACTCCAGTG 2220	B 8		1081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTGGTGCTGATGGCAACCAAC
2101 ATGGGTTACAGGATTTACCAAGAATTTGAAGTAACTGTACCTGATTCTATCACTTCTTGG 2160	B &		1021 AATGIGTTCITCAAGCAACATGATTACATCATTGAGITTTTTGATTATACTACTGTCTTG 1080
2041 GGTAGCAGTCCACATGTCCGAAAGCATTTTCCAGAGACTTGGATTTGGCTAGACACCAAC 2100	B &	•	961 GTAGAAATTTTAACCACAGTGACAGAATCAGTTACAGGTATTTCAAGAAATGTAAGCACT 1020
1981 GCTGAGAGGTTTATGGAGGAAAATGAAGGACATATTGTAGATATTCATGACTTTTCTTTG 2040 	g dy		901 AATGTAATGGATTCTTCAAATGGACTTTCTGAATACCTGGATCTATCT
1921 TTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTTATGACAATGCAGAATAT 1980 	dg Qy		841 ACAAAAACATTTAAGATAAATGGATCTGCAAACTTCTCTTTTAATGATGAAGAGATGAAA 900
1861 TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1920 	g Q		781 AAAGGAGACGTAACGCTTACATTTTTACCTTTATCCTTTTGGGGAAAGAAGAAAAAAATATT 840
1801 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGA 1860 	B 8		721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATATGGGAAGCCAGTG 780
1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT 1800 	р <i>Q</i>		661 GITTCAGAATAIGTATTACCAAAATTIGAAGIGACTITGCAGACACCATTATAITGTICI 720
1681 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAAGTCTCTCTTAGGATCTCTGTG 1740 	B 8		601 CTTGGTGACTGGTCTATTCAAGTTCAAGTGAATGACCAGACATATTATCAATCA
1621 GAPATTATAAGTGAIGTTCTAAAAATTCCIGTTCAGCTTGTTTTAAAAATAAGATAAAG 1680 	D Q		541 TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600
1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTAATTGTGTATTATATTGAAGATGATGGG 1620 	B &		481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG 540
1501 GTATCCAGGGGACAGTTGGTGGCTGTAGGAAAACAAAATTCAACAATGTTCTTTTAACA 1560 	Db .		421 AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTTAAGCCTTAC 480
	dg Qy		361 CGCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA
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The State of th	3540 AUTHORS Schuh, P TITLE Cd109 r 3652 JOURNAL Patent: SCHUH, P 3600 FEATURES	3480 ORGANISM Homo Eukaan 3592 Mamma 1 REFERENCE 1	ATGCAATTCTGGGTGTCATCAGAGTCCAAACTTTCTGACTCCTGGCAGCCACGCTCCCTG 3420		 ATGGAA	4373	4313	3120 Qy 4090 3232 Db 4253	3060 Qy 4030 3172 Db 4193	3000 Qy 3970 b 4133	2940 Qy 3910 2940 Db 4073 3052	4013	3953	3 8 9 3	3833 ATGGC	3773 CTGATT	GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT 2692
/mol type="denomic DNA"	,A. and Sutherland,R.D. nucleic acid molecules polypeptides and methods t: WO 02070696-A 5 12-SEP-2002; Andre-(CA) - Sutherland, Robert D. (CA) Location/Qualifiers	Chordata; Craniata; Primates; Catarrhini	1938.1 GI:25261482 SAME CLED (**) 8apiens (human)	from Patent WO02070696.	CTTTGGCTGTGA 4450	TCAGGCTCCCATCACTATTACTTTACTTTACTTTCAAGCTTCTGTACTTT 4432	CUT CCTOT CARCELLI CONALGUES TENTE SE AGRETICA CONTROL SE AGRETICA CONTROL SE AGRETA	ATRIGIGATTACTATICAGCCARGGAGACAGGCGGTGAGAAGITACAACTICTOAAGITCAAGITCAGACTICTOAAGITCAGCCAAGITCAGACTICTOAAGITCAGCCAAGGAGAAGTAGAAACTCTGAAGTGAAGTG	GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC 4089	GASTATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGT 	TTAAGTIGGCTTTATIGGTIGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAAGTG TTAAGTGGCTTTATIGGTGCCTTCAGAAGCAATTTCTCTGAGCGAGACAGTGAAGAAAAGTG	GIGIGIACANGETITICGGGCCCGGGTAGGAGGIGCATGGCCTATAGGAAGTIAACCTA 3909	TITIGATI TAMAN GATI DE 19 I MANAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM	THE CAME TO THE CAME OF THE CAME AND THE CAM		CTGATTGACACACACACCACTTACTCTCAGACAGCAGAGCTTGCTGTGGTACAGCCACACGCTTACTTGCTAGTACAGCCAGATGTTTGTA	CTTGCTGTGCTACAGCCA 3669

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1081 AAGCCATCTCTCAACTTCACAGCCACTGTGAAGGTAACTCGTGCTGATGGCAACCAAC	Gaps 1;	98.5%; Score 4221.4; DB 0; ty 98.8%; Pred. No. 0; Mismatches 1; I	6. 12.
1021 AATGTGTTCTTCAAGCAACAIGALLACAICAICAICAICAICAICAICAICAICAICAICAICAI			
961 GTAGAAATTTTAACCACAGTAGATTACAGGTATTTCAAGAAATGTAAGCACT 1020		VSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCKFCEDGASGERIE	00
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721 ATGAATTCTAAGCATTTAAATGGTACCATCACGGCAAAGTATACATTACATGTAGGAAGCATTAAATGGTACCATCACGGCAAAGTACATACA	ILSYMVVSRGQLVA VFKNKIKLYWSKV HELELYNTGYYLG Db	VTÓRNYTELEMPOSNOVENENT KYGS PELIVVSGNIKYELENYKYKKIKYKYKYKYKYKYKYKYKYKYKYKYKYKYKYKYK	
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22	APGIIRPGGNVTI LPSLPLNSADEIY FRIVTLFSDFKPY Db	/ db_ xret="d1.200000; / translation="mdgrpil/raahil/cvctaalavapgeretyttabelikeggnvti / gveilhergovtykabilkyrasnil/cvctaalavapgeretyttabelikeggrkyt / gveilhergovykabilkyrasnil/cvctaalavapgeretykegivil	
		/codon_start=1 /protein_id="CAD57496.1" /protein_id="CAD57496.1"	
541 TCACAACAAAGIGAICTIGGAGICATTICCAAAACTTITCAGCTATCTTCCCAICCAATA 600	y Q		CDS
81 AAAACCTCTTTAAACATTCTCATTAAAGAACCCCATTAAAACCTATCTTCCCATCCAATA	Db	/OLYGERS TO THE PROPERTY OF TH	
481 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGIGGIGGTTG 540	Qy		FEATURES source
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GCTTATCATTTGAGACCAAGAGAATATCTGTCTTCATTCA	Euteleostomi; Qy; Homo.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae	ORGANISM
301 ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC 300	מם	Homo sapien	KEYWORDS
ATTTATGAGCTACGTGTAACCGGACGTACCCCAGGATGAGATTTTATTCTCTAATAGTACC 36	Qy	1 GI:2526953	ACCESSION VERSION
241 GARANGGOTCTTTTRAWACACTIAC TO THE TOTAL THE HILLIAND THE HILLIAND THE TRAWACACTT TO THE TOTAL	PAT 23-NOV-2002 QY	AX537610 4335 bp DNA linear PAT	AXS37610
GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGAACAGCAGAAGAGAGAG	סט		
	VQ	ATGGAACTTTGGCTGTGA	Db 4433
121 AATGTGACTATTGGGGTGGAGCTTCTGGAACCTGCCCTTCACAGGTGACTGTGAAGGCC 180		TCAGGCTCCCATCATCA	
GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAG-s-a-1	4432		Qy 4210
61 GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGCCCCGGAGGA 120			Qy 4150 Db 4313
1 ATGCAGGGCCACCGCTCCTGACCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG 60	GGAGCT 4209		
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3241 AGAGGAATTTCAGACAATTATACTCTAGCCCTTATAACTTATGCATTGTCATCAGTGGGG .3300 	— ОУ ОУ	2161 GTGGCTACTGGTTTTGTGATCTCTGAGGACCTGGGTCTTGGACTAACAACTACTCCAGTG 2220	. 8
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GGCAATAAAA GGCAATAAAA	p & &	41	B 8
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3001 CCTTACATAGATATTGATCAGAATGTGTTACACAGAACATACACTTGGCTTAAAGGACAT 3060 	da VQ	1921 TTGACAGATGCAAACCTCACGAAGGATTATATTGATGGTGTTTATGACAATGCAGAATAT 1980 	g Q
2941 GACCCTTCTGGGAGCACTTGGTTGTCAGCTTTTGTTTTAAGATGTTTCCTTGAAGCCGAT 3000	Qy Db	1861 TATTATTTAGGCATGTTCATGAATTCTTTTGCAGTCTTTCAGGAATGTGGACTCTGGGTA 1920 	Db Qy
2881 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTTGGGAATTAT 2940	Qy Db	1801 GCCTCTAATGATATTACAATGGAAAATGTGGTCCATGAGTTGGAACTTTATAACACAGGÁ 1860 	Db Qy
2821 AAAAAGAACAACTGACAGATAATTTGAAAGAAAAAGCTCTTTCATTTATGAGGCAAGGT 2880 	. Ob	1741 ACACAGCCTGACTCCATAGTTGGGATTGTAGCTGTTGACAAAAGTGTGAATCTGATGAAT 1800	gb Qy
2761 TGTGGTGAACAGAACATGATAAATTTTGCTCCAAATATTTACATTTTGGATTATCTGACT 2820 	Оу Db	1681 CTATATTGGAGTAAAGTGAAAGCTGAACCATCTGAGAAGTCTCTTTAGGATCTCTGTG 1740	p Q
2701 GGAGATGTTCTTGGTCCTTCCATCAATGGCTTAGCCTCATTGATTCGGATGCCTTATGGC 2760	da Vy	1621 GAAATTATAAGTGATGTTCTAAAAATTCCTGTTCAGCTTGTTTTTAAAAATAAGATAAAG 1680 	dd Qy
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2581 TCACAATCCATCTTATTAGACTTGACAGATAGGCTACAGAGTACCCTGAAAACTTTG 2640	Db Qy	2 2	Db Qy
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                                                                          4261
                                                                                                                                                            42915 CTGTCCTCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT
                                                                                                    4210\TCAGGCTCCCATCATCACTCTTCAGTCATTTTATTTTCTGTTTCAGCTTCTGTACTTT 4269
4270 AIGGAACTIIGGCIG 4284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGATTGACACACACACCGCTTACTCCTTCAGACAGCAGAGCTTGCTGTGGTACAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAATCCCAATTATGAGGTGGCTAAGCAGGCAAAGAAATAGCTTGGGTGGTTTTGCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTGTACAAGCTTTTCGGGCCCGGGTAGGAGTGGCATGGCTCTTATGGAAGTTAACCTA 3909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTGATTTAGATGTTGCTGTAAAAGAAAATAAAGATGATCTCAATCATGTGGATTTGAAT 3849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAAATCAAGAAGCC 3840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATAATGTGAAGGCTTCTGGGTCTTCTAGAAGACGAAGATCTATCCAAAAATCAAGAAGCC 3789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGCAGTTAATATTTCCGGCAAATGGTTTTGGATTTTGCTATTTTGTCAGCTCAATGTTGTA 3729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAAGGACAAATATCCAAGTGACCGTGACGGGGCCTAGCTCACCAAGTCCTGTAAAGTTT 3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTCAGGATACCACTGTGGCTTTAAAGGCTCTGTCTGAATTTGCAGCCCTAATGAATACA
                                                                                                                                                                                                                                                                                                                                                                           GTTÄÄTÄTTCCTGCTGÄGÄÄÄACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTAATATTCCTGCTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC 4089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATATGATCATGGAAAACTCAACCTCTATTTAGATTCTGTAAATGAAACCCAGTTTTGT
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                                                                     -CTTGCTGTGGTACAGCCA: 3669
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181 GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT 240

AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG

121 121

61 61

GCCGTGGCTCCCGGGCCTCCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA 120

GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCCGGAGGA

120

180 180 ATGCAGGGCCCACCGCTGACCGCCCCCCCCCCTCTGCGTGCACCGCCGCGCTG ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG

60 60 1.

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Matches 4282;

Conservative

0;

Query Match Best Local Similarity

98.4%;

Score 4219.8; Pred. No. 0; 0; Mismatches

DB 6; Length 2

4335;

Indels

51;

Gaps

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SRE RY 6
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AUTHORS
TITLE
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ORGANISM
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VERSION
KEYWORDS
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AX537612
BASE COUNT
ORIGIN
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Sequence 3 from Patent WO02070738.
AX537612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schuh, A. and Ouwehand, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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VRQRVYTEYWSGSNSGNQKMEAVQKINVTVPQQGTFEKLEFFILEDSSELQLKAFLGS
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MEMNSFAVPQBCGLMVLITDANLTKNITOFVINDATYAERFMEENEGHIVDIHDFSLGS
SPHVRKHPPETMIMLDTNMGSRIYQEEEVTVEDSITSWVATGFVISBDLGLGITTTPU
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INATGHQOTLAGATVLFFIRFTHLGEIDITTAGATVAGATVAGATVAGATV
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KTSLNILIKDPKSNLIQQWLSQQSDLGVISKTFQLSSHFILGDRSIQVQVNDQTYYQS
FQVSBXYLLFXFEVTLQFFLYCSMQSKHLNGTITAKYTYKFKDVKGDVTLFLFLSFKFK
KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGFVEILTTVTESVTGI
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                                                                                                                                                                                                                                              GRVIHSELQGGNKSPVTLTAYIVTSLLGYRKYQPNIDVQESIHFLESEFSRGISDNYT
LALITYALSSVGSPKAKEALNMLTWRAEQEGGMQFWVSSESKLSDSWQPRSLDIEVAA
YALLSHFLQFQTSEGIPIMRWLSRQRNSLGGFASTQDTTVALKALSEFAALMNTERTN
IQVTVTGPSSPSPVKFLIDTHNRLLLQTAELAVVQPMAVNISANGFGFAICQLNVVYN
                                                                               VSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHHSSVIFIFCFK
LLYFMELWL"
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SFSAFGNYDPSGSTWLSAFVLRCFLEADPYIDIDQNVLHRTYTWLKGHQKSNGEFWDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAD57497.1"
/db_xref="GI:25269536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DN
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens'
/mol type="genomic DNA"
                                                                                                                                                               VKASGSSRRRSIQNQEAFDLDVAVKENKDDLNHVDLNVCTSFSGPGRSGMALMEVNL
LSGFMVPSEAISLSETVKKVEYDHGKLNLYLDSVNETQFCVNIPAVRNFKVSNTQDAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translation="MQGPPLLTAAHLLCVCTAALAVAPGPRFLVTAPGIIRPGGNVTI"
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                                   922 g
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ANK (USPTO)

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Result
No.
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Maximum Match 100%
Listing first 45 8
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
                                                                        4224.4
4224.4
4224.4
4223.4
                                                                                                                                                                 4281.2
                                                                                                                                                                                                            Score
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seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                         N Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
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                    24-APR-2002; 2002WO-CA00560
                                         31-OCT-2002
                                                       WO200285942-A2
                                                                                                                                                                                             Human r150 gene #1.
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C. elegans alpha-2
C. elegans alpha-2
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24-APR-2001; 2001US-285713P. 14-FEB-2002; 2002US-356163P.

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Matches 4283;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel transforming growth factor (TGF)-beta 1 binding reagent which comprises r150 protein which acts as accessory receptor of TGF-beta, useful for negatively madulating TGF-beta activity, and thus for
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New CD109 nucleic acids and polypeptides, useful in gene therapy, particularly for treating strokes, myocardial infarctions, thromb thrombocytopenia, autoimmune diseases, or organ or bone marrow transplantation -
                                                                                                                                                              WPI; 2002-713450/77.
P-PSDB; ABB82165.
                                                                                                                                                                                                                                                                                                                         (SCHU/)
                                                                                                                                                                                                                                                          Schuh A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CD109; alpha2 macroglobulin; thioester; cerebroprotective; cardiant; immunosuppressive; haemostatic; anticoagulant; thrombolytic; human; cardiovascular; vasotropic; gene therapy; CD109 Kl; gene; ss.
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SUTHERLAND
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/product= "CD109 K1"
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CC for treating or detecting a disease or disorder, e.g. conditions
CC associated with endothelial activation, platelet activation, activation
CC of the coagulation or fibrinolytic systems, activation of T lymphocytes
CC and of the complement system, quantitative or qualitative abnormalities
CC of platelet function, increased or impaired platelet aggregation and
CC activation, increased or impaired activation of the coagulation and/or
CC fibrinolytic systems, or impaired or increased immune activation. These
CC are also useful for treating cardiovascular disorders, stroke, myocardial
CC infarction, thrombosis, embolism, peripheral vascular disease,
CC transplantation, or bone marrow transplantation. The CD109 nucleic acids
CC or their antisense nucleotide sequence are useful in gene therapy for
CC Creating these conditions. The present sequence represents the human
CC CL109 K1 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptides. These nucleic acid molecules include the human cDNA sequences comprising CD109 K1, CD109 K1-H7, CD109 K15 or their variants. CD109 is a novel member of the alpha2 macroglobulin (alpha2M)/C3, C4, C5 family of thioester-containing proteins. The CD109 polypeptides can be expressed by standard recombinant methodology. The CD109 nucleic acid, CD109 polypeptide or its mimetic, or the anti-CD109 antibody is useful
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Sequence 4761 BP; 1420 A; 912 C; 1016 G; 1413 T; 0 other;

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문 S 밁 S 밁 Ś 밁 Ş र् 뭐 밁 S 밁 S 밁 ş 문 S Ş 문 밁 Query Match Best Local Similarity Matches 4286; Conserv 661 109 653 593 481 421 473 361 413 301 353 241 293 181 233 121 173 113 61 GTTTCAGAATATGTATTACCAAAATTTGAAGTGACTTTGCAGACACCATTATATTGTTCT TCACAACAAAGTGATCTTGGAGTCATTTCCAAAACTTTTCAGCTATCTTCCCATCCAATA 600 AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG AAGCCAAAGCAAGAAGTGAAGTTTCGCATTGTTACACTCTTCTCAGATTTTAAGCCTTAC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTTACCTCTGAACAGTGCAGATGAG AAAACCTCTTTAAACATTCTCATTAAGGACCCCAAATCAAATTTGATCCAACAGTGGTTG **AAGCCAAAGCAAGAAGTTTCGCATTGTTACACTCTT** ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC GAAAAAGGCTCTTTTAAGACACTTACTCTTCCATCACTACCTCTGAACAGTGCAGATGAG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGATCATCAGGCCCGGAGGA 120 ATGCAGGGCCACCGCTCCTGACCGCCGCCCACCTCCTGCGTGTGCACCGCCGCGCTG GAGCTGCTCAAGACAGCATCAAACCTCACTGTCTCTGTCCTGGAAGCAGAAGGAGTCTTT **AATGTGACTATTGGGGTGGAGCTTCTGGAACACTGCCCTTCACAGGTGACTGTGAAGGCG** Conservative 98.5%; 0; Mismatches Score 4224.4; Pred. No. 0; DB 24; Length 4761; 1; Indels CAGATTTTAAGCCTTAC 51; Gaps 660 720 652 540 592 480 532 420 360 240 180 232 172 472 412 300 352 292 60

Claim 1; Fig la; 156pp; English

The invention relates to isolated nucleic acid molecules encoding CD109

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Database :
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ALIGNMENTS

TITLE JOURNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AX534934	RESULT 1
Cd109 nucleic acid molecules polypeptides and methods of use Patent: WO 02070696-A 1 12-SEP-2002;	Schuh, A. and Sutherland, R.D.	Mammaila; Eucheria; Primates; Catarrhini; Hominidae; Homo. 1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; .	Homo sapiens	Homo sapiens (human)		AX534934.1 GI:25261474	AX534934	1 from Patent W002070696	AX534934 4761 bp DNA linear PAT 22-NOV-2002	•	

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Homo sapiens CD109 (CD109) mRNA,
AF410459
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                                                                                                                                                                        Lin,M., Sutherland,D.R., Horsfall,W., Totty,N., Yeo,E., Nayar,R. Wu,X.F. and Schuh,A.C.
Cell surface antigen CD109 is a novel member of the alpha(2)
macroglobulin/C3, C4, C5 family of thioester-containing proteins
Blood 99 (5), 1683-1691 (2002)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                    Direct Submission
Submitted (14-AUG-2001) Medicine, U
College Circle, Room 7366, Toronto,
                                                                        Lin, M., Sutherland, D.R., Horsfall, W., Wu, X.-F. and Schuh, A.C.
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ATTTATGAGCTACGTGTAACCGGACGTACCCAGGATGAGATTTTATTCTCTAATAGTACC
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4748
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3301 AGTCCTANAGCGAAGGAAGCTTTGAATATGCTGACTTGGAGAGCAGAACAAGAAGGTGGC 3360	3173 CAGANATICCAACGTGAATTTTGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT 3232 3121 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCCTCCTGGGATATAGA 3180	2881 TACCAGAGAGAACTTCTCTATCAGAGGAAGATGGCTCTTTCAGTGCTTTTTGGGAATTAT 2940	2521 GCTTCTGATGCTGTCACCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAATCATAT 2580
RESULT 3 AX534938 LOCUS DEFINITION Sequence 5 from Patent WO02070696. ACCESSION AX534938 VERSION AX534938 VERSION AX534938.1 GI:25261482 KEYWORDS SOURCE ORGANISM Homo sapiens (human) ORGANISM EUKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS TITLE JOURNAL FEATURES SCHUH, A. and Sutherland, R.D. TOCANIAL FEATURES SCHUH, Andre (CA) - Sutherland, Robert D. (CA) FEATURES SOURCE /mol_type="genomic DNA"	4150 CTGTCCCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT 4160 CTGTCCCCCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT 4110 CTGTCCTCCTGTGACCTTTCCAGTGATGTCCAGGGCTGCCGTCCTTGTAGGATGGAGCT 4210 TCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAGGCTTCTGTACTTT 4210 TCAGGCTCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAAGCTTCTGTACTTT 4210 ATGGAACTTTGGCTGTGA 4287 4270 ATGGAACTTTGGCTGTGA 4287 4433 ATGGAACTTTGGCTGTGA 4450	Db 17AAGIGGATTACTATGAGGCAAAACTTTAAAGTTTCAAATGCAAAGTCAAGTGAAAGCAAGTTACTAAAGTGCAAAGCAAGTTACTAAAGAAAG	3601 GAAAGGACAAATATCCCAAGTGACCGTGACCGAGGCCTAGCTCACCAAGTCCT

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1981 GCTGAGAGGTTTATGAGGAAATGAAGGACATATTGTAGACTATTCTTTG 1981 GCTGAGAGGTTTATGAGGAAAATGAAGGACATATTGTAGACTTTTCTTTG 2041 GGTAGCAGTCCACATGTCCGAAAACTGAAGGACATATTGTAGATTTTGTAGACACTTTCTTT	801 861 861 921 921	681 741 741 801	1561 CCAGAAAATTCTTGGACTCCAAAAGCCTGTGTCCACTTGTTTTTTTT	501 0			1081 AAGCCATCTCCAACTTCACAGCCACTGTGAAAGTAACTGTGCTGATGCCAACCAA
Trg 2040 Trg 2040 Trg 2040 Trg 2040 Trg 2040 Trg 2040 Trg 2040 Trg 2040 Trg 2040 Trg 2040 Trg 2040 Trg 2020	1860 1920 1920 1980	1740 1740 1800 1800	1620 1620 1680 1680	GTA 1500 CY	1380 1380 1440	1260 1260 1320 1320	
3061 CAGAATTCCAACGTGAATTTTGGGATCCAGGAGAGAGTGATTCATAGTGAGCTTCAAGGT 3120 3061 CAGAATCCAACGGTGAATTTTGGGATCCAGGAGAGAGTGATTCATAGTGAGCTTCAAGGT 3120 3061 CAGAATCCAACGGTGAATTTTGGGATCCAGGAAGAGTGATTCATAGTGAGCTTCAAGGT 3120 3121 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTGTAACTTCTCCTCTGGGATATAGA 3180 3121 GGCAATAAAAGTCCAGTAACACTTACAGCCTATATTTTTAGACTTCTCTCTC	1881 TACCAGAGAGAACTTCTCTATCAGAGGGAAGATGGCTCTTTCAGTGCTTTTGGAACTATTAT 1941 GACCCTTCTGGAGGCACTTGGTTGCAGCTTTTTAAGATGTTTCCTTGAAGCCGAT 11	TAG	641 701 701	2521 GCTTCTGATGCTGATCCCAGATGATTTTAGTAAAGGCTGAAGGAATAGAAAAATCATAT 2580	19 19 10	281 281 341 341	221 GJ

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                                                                                                                                                                                                                                                                                                                                                                                                    4030 GTTAATATTCCTGCTGTGAGAAACTTTAAAGTTTCAAATACCCAAGATGCTTCAGTGTCC
                                                                                                                                                                            BA; CTGTCCTCTGTGACCTTTGCAGTGATGTCCAGGGCTGCCGTCCTTGTGAGGATGGAGCT
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                                                                                                           TCCCATCATCACTCTTCAGTCATTTTTATTTTCTGTTTCAAGCTTCTGTACTTT
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AX537612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                            KAEPSEKVSLRISVTOPDSIVGIVAVDKSVNLMMASNDITMENVVHELELYNTGYYLG
MEMNSFAVFQECCLWYLTDANLTKDYIDGVVDNAEYAER FMEENGGHIVDIHDFSLGS
SPHVRKGFPERFMIWLDTHMGSRIYOGEFEVTVDSITSWAATGFVISEDLGLGTTTPY
ELQAFQPFFIFLNLPYSVIRGEEFALEITIFNYLKDATEVKVIIEKSDKFDILMTSNE
INATGHQOTTLLVPSEDGATULFPIR PTHLGEIPITVTALSFTASDAVTOMILVKAEGI
EKSYSQSILLDLTDNRLOSTILKTLSFSFPENTVTGSERVQITAIGDVLGPSINGLASL
IRMPYGCGEDQNNINFAENIYILDYLTKKKQLTDNLKEKALSFRRQGYQRELLVQREDG
EFSAFGNYDBSGSTMLSAFNIYILDYLTKKKQLTDNLKEKALSFRRQGYQRELLVQREDG
GFSAFGNYDBSGSTMLSAFNIYLDYLTKKKQLTDNLKETHTLKGHQKSNGEFMDP
GRVIHSELQGGNKSPVTLTAYIVTSLLGYPKYDNIDVGESIHFLESEFSRISDNYT
LALITYALSSVUSPKAKEALNNLTWARAEGEGASTODTTVALKALSEFAALNNTERTN
YALLSHFLOFGTSEGIPIMRMISRORNSLGGFASTODTTVALKALSEFAALNNTERTN
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ELRVTGRTQDEILFSNSTRLSFETKRISVFIQTDKALYKPKQEVKFRIVTLFSDFKPY
KTSLNILIKDPKSNLIQQWLSQQSDLGVISKTFQLSSHPILGDWSIQVQVNDQTYYQS
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KSSMAVHSLFKSPSKTYIQLKTRDENIKVGSPFELVVSGNKRLKELSYMVVSRGQLVA
VGKQNSTMFSLTPENSWTPKACVIVYYIEDDGEIISDVLKIPVQLVFKNKIKLYMSKV
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KKNITKTFKINGSANFSFNDEEMKNVMDSSNGLSEYLDLSSPGPVEILTTVTESVTGI
LLYFMELWL"
                                                                                                   VKASGSSRRRRSIQNQEAFDLDVAVKENKDDLNHVDLNVCTSFSGPGRSGMALMEVNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens'
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/db_xref="taxon:9606"
                               VSIVDYYEPRRQAVRSYNSEVKLSSCDLCSDVQGCRPCEDGASGSHHHSSVIFIFCFK
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                                                                                                                                      IQVTVTGPSSPSPVKFLIDTHNRLLLQTAELAVVQPMAVNISANGFGFAICQLNVVYN
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Query Match Best Local Similarity 98.4%; Score 4219.8; Pred. No. 0;

Conservative 0; Mismatches DB 6; 2; Length 4335;

51;

Gaps

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1 ATGCAGGGCCCACCGCTCCTGACCGCCGCCCACCTCCTCTGCGTGTGCACCGCCGCGCTG GCCGTGGCTCCCGGGCCTCGGTTTCTGGTGACAGCCCCAGGGGATCATCAGGCCCGGAGGA 120, GCCGTGGCTCCCGGGCCTCCGGTTTCTGGTGACAGCCCCCAGGGATCATCAGGCCCCGGAGGA 120 ATGCAGGGCCCACCGCTGACCGCCGCCCACCTCCTGCGTGCACCGCCGCGCGCTG

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Team: OIPEBackFileIndexing

Dossier: 09915515

Legal Date: 01-05-2004

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